STIC-Biotech/ChemLib

From: Sent:

Mertz, Prema

Wednesday, September 25, 2002 2:48 PM STIC-Biotech/ChemLib

To: Subject:

09/904,954

Please search SEQ ID NO:1, 3, wit DNA databases.

Please searc SEQ ID NO:2, 4 with protein databases.

Thanks

Prema Mertz, Ph.D. Primary Examiner
Art Unit 1646
Crystal Mall 1, Room 10E-01 United States Patent & Trademark Office # (703) 308-4229

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

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AC021890 Homo Sapi AB051678 Danio rer AY045577 Rattus no U92885 Mus musculu

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Searched:

AR134682 Sequence AR152043 Sequence U92894 Homo sapien AC004258 Homo šapi X90377 G. domesticu AR134677 Sequence AR152038 Sequence

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1 (bases 1 to 1037)
Beckmann, M. Patricia, and Cerretti, D. P.
Cytokines that bind the cell surface receptor hek
Patent: US 5738844-A 1 14-APR-1998;
Location/Qualifiers
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AR048795 Sequence AR103236 Sequence I56902 Sequence 11 I88172 Sequence 11

AF131912 Rattus no AC073818 Mus muscu U31204 Xenopus lae

r09669 D.rerio mRN

PAT 04-DEC-1998

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Score 1037; DB 6; Length 1037; Pred. No. 1.8e-151;

100.0%; 100.0%;

Query Match Best Local Similarity

Description

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Score Match Length DB

Result

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l (bases I to 1037)
Beckmann, M. Patricia and Cerretti, D. Antibodies that bind hek ligands
Patent: US 5969110-A I 19-OCT-1999;
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                              1037 bp
from patent US 5969110.
                                                                                                                      Location/Qualifiers
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343 c 337 g
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/note="Vector: pCMV-SPORT6"
71. .787
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                    1769 bp
ephrin-A3, clone N
                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                     BC017722.1 GI:17389356
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GICTCGTTCCAGGTCC 1037
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JOURNAL
          1021
                                   RESULT
BC017722
                                                                             ACCESSION
                                                                                     VERSION
KEYWORDS
SOURCE
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Length 1037;
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Score 1037; DB 6;
Pred. No. 1.8e-151;
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REHLPLAVGIAFFLMTFLAS"
1 577 c 314 g 335 t
D mRNA linear PRI 06-DEC-2001
MGC:21335 IMAGE:4397263, mRNA,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1769)
                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information can be for http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution
through the I.M.A.G.E. Consortium/LLNL at:
Series: IRAK Plate: 27 Row: d Column: 19.
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Pred. No. 4.7e-144;
D; Mismatches 2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 987)

Kozlosky, C. J. Maraskovsky, E., McGrew, J.T., VandenBos, T., Teepe, M. Lyman, S.D., Srinivasan, S., Fletcher, F.A., Gayle, R.B. III, Cerretti, D.P. and Beckmann, M.P.

Ligands for the receptor tyrosine kinases hek and elk: isolation on CDNAs encoding a family of proteins
Oncogene 10 (2), 299-306 (1995)
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glycosyl-phosphatidylinositol (GPI)
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Pred. No. 9.9e-144;
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Cerretti, D. P.
Direct Submission
Submitted (01.5EP-1994) Immunex Corp.,
WA 98101, USA
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1. .987
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329 c 323 g
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Human receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA, complete
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VERSION KEYWORDS SOURCE ORGANISM

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GAGATCCATTGTGCTGGAAAGGCGGCGGCGGCTCCGGGGATGGCGGCGCGCTCCGCTGCTG
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Davis, S., Gale, N.W., Aldrich, T.H., Maisonpierre, P.C., Goldfarb, M. and Yancopoulos, G.D.
Method of enhancing the biological activity of Eph family ligands Patent: US 5747033-A 805-MAY-1998;
Location/Qualifiers
                                                                       540
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AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG
       CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGGAAGTGTCTGAGGATG
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                                                                                             CCCCTCCCCTGGGGGGGGGGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC
                                                                                                                                                                                                                                     TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC
                             TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGGCTACGAGTTCCACGCCGGC
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Pred. No. 2.1e-131;
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341 c 334 g
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96.3%; Pred
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Sequence 8 from patent
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AUTHORS
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HUMEFL2 758 bp mRNA linear PRI 09-NOV-1994 Homo sapiens (clone hEHK1-L) EHK1 receptor tyrosine kinase ligand (EFL-2) mRNA, complete cds.
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163
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TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG
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                                                                                       GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC
                                                                                                                                 AGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGCAGAGCAGTACGTG
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/translation="MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHL
RREGYTVQVNVNDYLDIYCPHYNSSGAGPGPGGAEQYVLYMVSRNGYRTCNASQGFK
RWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVF
VCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVFKLEKSISGTSFKREHL
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                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 758)
Davis,S., Gale,N.W., Aldrich,T.H., Maisonpierre,P.C., Lhotak,V.,
                                                                                                                     Pawson, T., Golfarb, M. and Yancopoulos, G.D.
Ligands for EPH-related receptor tyrosine kinases that require membrane attachment or clustering for activity
Science (1994) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             /product="EHK1 receptor tyrosine kinase ligand"
/protein_id="AAA52368.1"
/db_xref="GI:567004"
                                                                                                                                                                                                                                                                                                                                                              /gene="EFL-2"
/function="binds EHKl receptor tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                        /cell_line="SH-SY5Y"
/cell_type="neuroblastoma"
1, 758
/gene="EFL-2"
19, 723
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                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hEHK1-L"
                                                                 Eukaryota; Metazoa; Chordata;
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                                Homo sapiens cDNA to mRNA
Homo sapiens
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98.4%;
 L37360.1 GI:567003
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Mammalia; Butherlai Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 175826)

Marmalia; Butherlai Primates; Catarrhini; Hominidae; Homo.

Alsbrooks.S.L. Amaratunge, H.C., Ale. Banks, T., Barbaria, J.,

Bencon, J., Bingack, M., Brown, E., Brown, M., Bryant, N.P.,

Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Bowles, S. Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Burch, P., Burkett, C., Burrell, K.L., Bytd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Carter, M., Cavazos, S.R., David, R., Davila, M.L., Davis, C.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L.,

Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,

Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Edwards, C.C.,

Elanj, C., Escotto, M., Falls, T., Retraguto, D., Edwards, C.C.,

Elanj, C., Escotto, M., Falls, T., Retraguto, D., Edwards, C.C.,

Elanj, C., Escotto, M., Falls, T., Retraguto, D., Edwards, C.C.,

Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hane, S.,

Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,

Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,

Joudah, S., Karlsson, E., Howels, M., Leal, B., Lewis, L.C.,

Lewis, L., Li, Z., Lid, T., Ludy, T., Ludy, C., Liut, J., Ludy, M.,

Martinez, E., Massey, E., Marhiney, E., McLed, C., Liut, J., Luh, M.,

Martinez, E., Massey, E., Martin, R., Martindale, A.,

Martinez, E., Massey, E., Martin, R., Martin, R., Martinez, E.,

Martinez, E., Massey, E., Martin, R., Martin, R.,

Martinez, E., Massey, E., Martin, R., Martin, R., Martinez, E.,

Martinez, E., Massey, E., Martin, R., Welson, M., Stoney, J.,

Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,

Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, Stone, H., Sutcon, M., Sutcon, R., Wady, S., Wald, Mongon, M., Wady, S., Wald, Mongon, M., Wald, S., Wald, M., Wald, S., Wald, M., Wall, R., Wald, S., Walliams, G., Williamson, A., Walliams, G., Walliams, G., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC021890 175826 bp DNA linear HTG 10-NOV-2000
Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              ACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACG
                                                                                                                 GAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTG
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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                         Worley, K.C.
Direct Submission
Submission
Submitted (22-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2000 this sequence version replaced gi:9719697.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                           chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 144734 bases at least Q40
Consensus quality: 162873 bases at least Q30
Consensus quality: 165424 bases at least Q30
Estimated insert size: 170770; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-498A2
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Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamoto, H. Identification of ephtin-A3 and novel genes specific to the midbrain-MHB in embryonic zebrafish by ordered differential display Mechanisms of development. 107 (1-2), 83-96 (2001)
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Hirate,Y., Mieda,M., Harada,T., Yamasu,K. and Okamoto,H.
Direct Submission
Submitted (24-NOV-2000) Yoshikazu Hirate, Brain Science Institute,
RIKEN, Lab. of Developmental Gene Regulation; 2-1, Hirosawa,
Wako-shi, Saitama 351-0198, Japan (E-mall:hirate@brain.riken.go.jp,
Tel:81-848-467-9713, Fax:14-88-467-9714)
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Actinopterygii; Neopterygii<u>;</u> Teleostei; Euteleostei; Ostarlophysi;
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169967: gap of unknown length
171580: contig of 1613 bp in length
171680: gap of unknown length
172882: contig of 1202 bp in length
172982: gap of unknown length
174431: contig of 1449 bp in length
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Pred. No. 6.1e-45;
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Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB051678.1 GI:14196230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.4%;
                                                                                                                                                                                                                                       .175826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.4
Best Local Similarity 99.4
Matches 348; Conservative
  169868
169968
171581
171681
172883
172983
174432
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07-FEB-1998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                Euteleostomi;
                                                     1 (bases 1 to 355)
Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A.,
Jimenez,E., Varas,A. and Zapata,A.G.
Expression and function of the Eph A receptors and their ligands
ephrins A in the rat thymus
                                                                                                                                                                                                University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACCTGCAACGCCAGGCCATGAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGC 431
                                                                                                                                        2 (bases 1 to 355)
Munoz, J.J., Alonso-C.L.M., Sacedon,R., Crompton,T., Vicente,A.
Jimenez,B., Varas,A. and Zapata,A.G.
Direct Submission
Submitted (13-JUL-2001) Cell Biology, Complutense University of Madrid, Av. Complutense, Madrid 28040, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGCTACC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                               /note="Eph-related receptor tyrosine kinases ligand"
                          Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGCCCCATCAAGTTCTCGGAGAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACG
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                Vertebrata;
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Pred. No. 3e-28;
0; Mismatches 37; I
                Craniata;
                                                                                                                                                                                                                                    1. 355
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
<1. >355
                                                                                                                                                                                                                                                                                                                                                                                                              64
              Chordata;
                             Rodentia;
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             Eukaryota; Metazoa;
Mammalia; Eutheria;
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 Rattus norvegicus
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Best Local Simil
Matches 264; C
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                                                                     AUTHORS
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                                                                                                                                                     /translation="MALYALCLFLTTCTNFALVTAARHAVHWNSSNILLRKEGYTL
QVNVNDYLDIYCPHYNSSQRGIAEQYVLXMVSYRGYRTCDPQLGFKRWECNRPHAPHA
PIKFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHHGRSCLRLRVYVCCSTASDSDDE
PQPTEPDYTLRPNIKIDDLDDYDNFEVPKLEKSISGSSPSRDRLLTYASLLLIALSV
S"
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                                                                                                                                                                                                                                                                                                                                                                                                                           732
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                                                                                                                                                                                                                                                                                                                                                       CITCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCAC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 TCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCCCCCTCCACATC 594
                                                                                                                                                                                                                                                                                                                                        CCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGT 234
                                                                                                                                                                                                                                                                                                                                                                                               GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 GGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACATGGT 354
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                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                   Length 1838
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Pred. No. 4.2e-30;
0; Mismatches 155; Indels
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Rattus norvegicus ephrin A3 mRNA, partial cds.
AY045577
                                                                                                                                                                                                                            469
                                                                                                            /product="ephrin-A3"
/protein_id="BAB55891.1"
/db_xref="G1:14196231"
           /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                            ь
                                                     /gene="ephrin-A3"
                                                                  550. .1209
/gene="ephrin-A3"
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68.0%;
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AC104632.2 GI:17998594
HTG; HTGS_PHASEI; HTGS_DRAFT.
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2155: gap of u
4235: contig o
6526: contig o
6626: gap of u
9454: contig o
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                  505 CCACGAGTACTACTACATCT
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                                                                                                                                                                         house mouse.
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AC104632/C
                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                /protein_id="AAC39961.1"
/db_xref="GI:2843099"
/translation="LRREGYTVQVNVNDYLDIYCPHYNSSGPGGGAEQYVLYMVNLSG
                                                                                                                                                                                                                                                                                                                                  YRTCNASQGSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGOËYYISTPTHN
LHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKS
ISGTSPKREHLPLAVGIAFFLMTLLAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
1 (bases 1 to 2535)
Cerretti,D.P. and Nelson,N.
Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
Conservation of intron/exon structure
Genomics 47 (1), 131-135 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076 CAGCCAAGGCTCCAAGCGTGGGAATGCAACCGGCAGCACGCCTCGCACACGCCCCATCAA 1135
                                                                                                                                                                                                                                        join(<926. .1215,1543. .1608,1793. .1870,2111. .2241)
/gene="Epl3"
/note="GPI-anchored ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGGCCGGGGCCCGGAGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 CGGGCCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCCACCACCATCAA 444
                                                                                                                                                                                                                                                                                                                                                                                            Join(<926. .1215,1543. .1608,1793. .1870,2111. .2535)
/gene="Epl3"
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                                                                                                           Direct Submission
Submitted (11-MAR-1997) Molecular Biology, Immunex Corp.,
University Street, Seattle, WA 98101, USA
Location/Qualifiers
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Pred. No. 2.6e-25;
0; Mismatches 25;
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/db_xref="taxon:10090"
/chromosome="3"
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Cerretti, D.P. and Nelson, N.
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AC104632 289579 bp DNA linear HTG 29-DEC-2001
Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
SEQUENCE, 72 unordered pieces.
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Hua,A. and Roe,B.A.

Direct Submission

Submitted (15-DEC-2001) Department of Chemistry And Blochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

ON DEC 29, 2001 This sequence version replaced g1:17861055.

Center: Department of Chemistry And Blochemistry
The University of Oklahoma
                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 289579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING DRAFT
SEQUENCE, 66 unordered pieces.
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Submitted (10-DEC-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
Ok 73019, USA
On Dec 24, 2001 this sequence version replaced gi:17439220.

Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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Rusaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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Muse And Roe, B.A.

Mus musculus BAC Clone rp23-295a4
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus. 1 (289579)
Hua,A. and Roe,B.A.
                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mus musculus clone rp23-368024 strain C57BL/6J, WORKING DRAFT
SEQUENCE, 72 unordered pieces.
AC104632
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21.4%; Score 222; DB 2; Length 326750;
Best Local Similarity 84.7%; Pred. No. 1.2e-25;
Matches 271; Conservative 0; Mismatches 25; Indels 24;
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16.5%; Score 171.2; DB 2; Length
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Human AL-1 CDNA.
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Seq ID No: 8 of WO

Human cell cycle a Rat differential t Drosophila melanog Mycobacterium tube

us-09-904-954-1.rng

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Run on:

Sequence:

Searched:

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Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
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AAI99683
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AAK51628
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7.1429 a

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7.1429 b

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7.1429 c
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93US-0114426.
93US-0161132.
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 03-OCT-1995 (first entry)
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30-AUG-1993;
03-DEC-1993;
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Human secreted pro
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CDNA encoding an a
Mouse Elf-1 cDNA.
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7447.983 Million cell updates/sec
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                                                                                                                                             1 GGATCTTGGAACGAGACGAC......GTCGTCTCGTTCCAAGATCC 1037
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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LERK-6 exon.

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12-APR-1994;
01-SEP-1994;
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                                                                                                                                                               The sequence is that of a clone encoding hek-L protein, a protein that can blind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for hek proteins, to purify hek proteins, and to carry diagnostic or cytocoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors.
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                                                                                                                                                                                                                                                                                                                      Length 1037;
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100.0%; Pred. No. 1.2e-186;
ive 0; Mismatches 0;
                                                                                                                                           Claim 1; Page 34; 45pp; English
 94US-0240124
                                            DP;
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                                            Cerretti
                      (IMMV ) IMMUNEX CORP
                                                                 WPI; 1995-106811/14.
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                            P-PSDB; AAR71481
                                           Beckmann MP,
09-MAY-1994;
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                     CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG
                                                                                               Ligands which bind Eph family receptors - used in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                             L; Eph transmembrane tyrosine kinase family ligand; disorder; identification; diagnosis; ss.
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94US-0222075.
94US-0229402.
94US-0299567.
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                                                                                       The DNA encodes an Eph transmembrane tyrosine kinase family ligand designated Ef1-2. Ef1-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
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                                                                                                                                                                                                                                                      Sequence 1070 BP; 196 A; 341 C; 334 G; 189 T; 10 other;
                                                                                                                                                                                                                                                                                                                          87.5%; Score 907.4; DB 16;
larity 96.3%; Pred. No. 3.2e-162;
Conservative 0; Mismatches 24;
                                           English.
                                             Fig 3; 58pp;
neurological disorders
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939; Conserv
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Best Local S:
Matches 939,
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA isolation;
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to 5'ESTs and for
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mapping
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Q
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mapping; ss.
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Gaps

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Indels

4.1e-30; thes 12;

19.8%; Scor. 94.7%; Pred. No. 4... 0; Mismatches

Similarity

Length 358;

DB 21;

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The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating custodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivaring agents attached to cells bearing than a trophic also be used as carriers for delivaring agents attached to cells bearing the elk or her elevance receptor. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                           LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease, neurodegenerative; excitotoxicity; ss.
CAGITCACCATGGGCCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC
                                                GTGTTCGTCTGCTCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCC
                                                                                                                                                                                                    CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCC 733
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                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                           Human LERK-6 polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                       AAX32767 standard; cDNA to mRNA; 642
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14.6%; Score 151.8; DB 20; Length 642;

Query Match

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73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTCGTGCCGTGCCGTT32
                                                                  GCTGCCGCTGCTGGCCCCAAGGGCCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
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                                                3 ggcgcccgcgcagcgcccgctgctcccgctgctcctgctgttaccgctgccgccgcc
                                                                                GCAGGTGAACGTGAACGACTATCTGGATATTACTGCCCGCACTACAACAGCTCGGGGGT
                                                                                                                                                                                                  229 -----ggggggcgccgctgccgccggccgagcgcatggagcactacgtgctgcatggt
                                                                                                                                                                                                                                          412 CAACCGGCCGCACGCCCCCACCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG
                                                                                                                                                                                                                                                                                           GAACAGCTCCAACCAGCACCTGCGGCGAGA-------GGGCTACACCGT
                                                                                                                                                                                                                                35 GAGCCGCAACGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG
                                                                                                                                                                                                                                                                                                              472 GGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACTTCT---CCAC
                                                                                                                                                                     183 ggaggtgagcatcaatgactacctggacatctactgcccgcactat-------
                                                                                                                                                                                         295 GGGCCCCGGGGCGGGACCGGGGCCCGGGGGCAGAGCAGTACGTGCTGTACATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor ligand; dementia; tachycardia; gene therapy; transgenic animal; ss; ds.
          Indels
61.0%; Pred. No. 6.2e-20;
cive 0; Mismatches 172;
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1471..1476
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/*tag= c
149..685
/*tag= d
686..783
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Best Local Similarity 61.0
Matches 340; Conservative
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diagnosis;
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5'UTR
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(first entry)

Location/Qualifiers

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/*tag=

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86..688

/*tag= b /product= Elf-1

/*tag= c 686..783 ..148

/*tag=

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Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Columns 73-76; 53pp; English.
                                                                                                 cDNA encoding an avian Elf-1 protein.
 AAV42927 standard; cDNA; 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheng H, Flanagan JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1994;
27-FEB-1995;
                                                                20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                sig_peptide
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                                                                                                                                                                                                                               Sallus sp
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                                  AAV42927;
                                                                                                                                                                                                                                                               Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                               3'UTR
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                                                                                                                                                                                                                                                                                                                                                            A chicken cDNA clone (AAT15009) codes for a novel EPH receptor ligand, Elf-1 (AAR84766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obd. from a day-3 chick embryo cDNA library using mouse Elf-1 cDNA (see AAT15008) as probe. The cDNA can be used for the prodn. of recombinant Elf-1, in the breeding of transgenic animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 ggtcaactacgagggccacgcgtcctgcgaccaccggcagaagggcttcaaacgttggga 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCAACCGGCCGCACGCCCCGCACACCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 gigcaaccggcccgactcccccagcggacccctcaagitctcagagaagitccagctct 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCAC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GCTGCTCGTGCCGTGCCGCTGCTGCTGCTGCCCAAGGGCCCGGAGGGCCCTGGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgaccccggcaaagtgatctc 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 ------ggagccgctgcccgccgagcgcatggagcgctacgtcctctacat 324
                                                                                                                                                                                                                                                           Murine and chicken EPH receptor ligand, {\rm Elf-1} - useful in diagnosis and treatment of disorders associated with the {\rm Elf-1} gene, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 149.2; DE 63.3%; Pred. No. 2e-19;
                                                                                                                                                                                                                                                                                                                            Claim 36; Page 87-88; 107pp; English.
                                                                                                                                                                                                                                                                                              dementia, tachycardia , etc.
                                                                                                              94US-0308814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.38;
                                                              95WO-US11869
                                                                                               95US-0393462
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                                                                                                                                                                               Cheng H, Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                           chicken cDNA clone
                                                                                                                                                                                                            WPI; 1996-188446/19.
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WO9609384-A1
                                                                                                            19-SEP-1994;
                                                              19-SEP-1995;
                                                                                               27-FEB-1995;
                                28-MAR-1996
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95US-0455001. 94US-0308814. 95US-0393462.

95US-0455001

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The present sequence encodes an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended in
                                                                                                                                                                                                                                                                                                                                                                                           transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGCCCAAGGGCCCCGGAGGGCCCTGGG 171
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Pred. No. 2e-19;
0; Mismatches 133; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;
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Best Local Similarity 63.3%;
Matches 276; Conservative
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                                         CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
                                                                                                      ggtcaactacgagggccacgcgtcctgcgaccaccggcagaagggcttcaaacgttggga 384
                                                                                                                                                 GGTGGCCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACAT
                                                                                         352 GGTGAGCCGCAACGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA
                                                                                                                  GTGCAACCGGCGCGCCCCGCACGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA
                                                                                                                                           CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCCAC
                 Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;
diagnosis; transgenic animal; ss; ds.
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                             Key
5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TGCTGCTCGTGCCCGTGCCGCTGCCGCTGCTGGCCCAAGGGCCCCGGAGGGGCCCTGG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                        A mouse cDNA clone (AAT15008) codes for a novel EPH receptor ligand, Elf-1 (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from an embryo mid- and hind-brain cDNA expression library using a receptor affinity probe technique with mek4-AP and sek-AP (AP = alkaline phosphatase) reagents. The cDNA is used for the prodn. of recombinant Elf-1, in the breeding of transgenic animals, the rhe design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                         Murine and chicken EPH receptor ligand, {\rm Elf}-1 - useful in diagnosis and treatment of disorders associated with the {\rm Elf}-1 gene, e.g. dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 cgagggagcgagcgcgcggcagcaccggggccatggcgccggcgcagcgccgctgctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 AGTACTACTACATCTCCACGCCCACTCACAACCT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a mammalian Elf-1 protein.
                                                                                                                                                                             Claim 36; Page 84-85; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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WPI; 1996-188446/19.
P-PSDB; AAR94777.
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Best Local Similarity
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           Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B651, LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a mammalian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 CGGGGGGGGGGGGGGGGGGCTCCGGGG--ATGGCGGCGCTCCGCTGCTGCTGCTGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 149.2; DB 1
62.6%; Pred. No. 2.1e-19;
                                                                                                                     Location/Qualifiers
1..264
4.tag= a
265..894
/*tag= b
//product= Elf-1
892..1809
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255.324
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1724..1729
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94US-0308814.
95US-0393462.
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Matches 322; Conservative
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P-PSDB; AAW71006.
                                                                   cone formation; ss
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27-FEB-1995;
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                                                   Isolated DNA encoding cytokine designated LERK-6 which binds to hek and elk cell surface receptors - useful for drug delivery and screening procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                          LERK-6; hek; elk; cell surface receptors; culture; reagent; neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
                                                                                   450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGGTTCCACGCCGGCCACG
                                                                                                                                                                                                                              353 ctgaccgatacgcagtctactggaaccgtagcaaccccaggtttcaggtgagcgctgtgg
                                         -----GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC
                                                                                                       cacacta-------cgggggcgccgctgccccggctgagcgcatgg
                                                                                                                                                                         --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCTCTCAAGTTCT
GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC
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/product= LERK-6 protein fragment.
                                                                                                                                                                                                                                                             510 AGTACTACATCTCCACGCCCACTCACAACCT 543
                                                                                                                                                                                                                                                                        AAT14010 standard; cDNA to mRNA; 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 2..313 /*tag= a
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P-PSDB; AAR91284.
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Claim 3; Page 36; 44pp; English.

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New cytokine designated LERK-6
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                                                                                                                                                                                              338
                                                                                                                                                                                                                                                                       455
                                                                                                                                                                                                                                                                               at-----ggggcgccgctgccgccggcgagcgtggagcattgagcact 125
                                                                                                                                                                                                                                            The LERK-6 polypeptide encoded by this sequence can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may
                                                                                                                                                        219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT
                                                                                                                                                                                             279 ACAACAGCTCGGGGGTGGGCCCCGGGGCGGGGCCCGGGAGGCGGGGGGCAGT
                                                                                                                                                                                                                                                                      AGTICCAGCGCTACAGCGCCTICTCTCGGCTACGAGTICCACGCCGGCCACGAGTACT
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                                                                                          Sequence 314 BP; 51 A; 108 C; 104 G; 51 T; 0 other;
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                                                                                                                    13.1%; Score 135.4; DB 1
1larity 70.9%; Pred. No. 7.3e-17;
Conservative 0; Mismatches 66
                                                                      be treated by contact with the polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exon sequence of human LERK-6.
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P-PSDB; AAY06821.
                                                                                                                              Similarity
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Matches 219;
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The invention relates murine and human LERK-6 polypeptides that bind to hak/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the hex or elk receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stable be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a conduction under different conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; Score 135.4; DB 20; 70.9%; Pred. No. 7.3e-17; ive 0; Mismatches 66;
Claim 3; Page 24; 46pp; English.
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Best Local Similarity 70.9's
Matches 219; Conservative
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us-09-904-954-1.rng

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The LERK-6 polypeptide encoded by this sequence can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may
                                                                                                                                                                                                                                                                                                  1 DNA encoding cytokine designated LERK-6 which binds to cell surface receptors - useful for drug delivery and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be treated by contact with the polypeptide.
                                   Location/Qualifiers
1..555
                                                                          /product= LERK-6
                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 33; 44pp; English.
                                                                                                                                                                                95US-0538709.
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                                                              /*tag=
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             musculus
                                                                                                    WO9610911-A1
                                                                                                                                                                                              05-OCT-1994;
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                                                                                                                                                                                                                                                Cerretti DP;
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                                                                                                                                                                                                                                           A fragment of murine Lerk-6 DNA was isolated by PCR for use as a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see AA713269). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCCACAGCCCCATCAAGTTCTCGGAGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geggeggetataccgtggaggtgagcatcaacgactacctggatatctactgcccacact 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a.....aggggggggggggcgctgccccggctgagcgcatggagcggt 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agttccaactcttcacccccttttccctgggctttgagttccggcctggccacgaatact 358
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                             New isolated human Lerk-7 cytokine - which binds to cell surface receptors elk, hek and eck, useful for delivering agents to cells or for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LERK-6; hek; elk; cell surface receptors; culture; reagent; neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTICCAGCGCTACAGCGCCTICTCTCTGGGCTACGAGTICCACGCCGGCCACGAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 128.8; DB 17; Length 67.7%; Pred. No. 1.3e-15; 1ve 0; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTACATCTCCACGCCCACTCACAACCT 543
                                                                                                                                                                                                                       Example 1; Page 34; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT14009 standard; cDNA; 555
                                   95US-0396946.
            95WO-US15781
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LERK-6 coding sequence.
                                                                         IMMV ) IMMUNEX CORP
                                                                                                                             WPI; 1996-287171/29.
                                                                                                                                            P-PSDB; AAW02587
            05-DEC-1995;
                                    01-MAR-1995;
                                                  06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-0CT-1996
                                                                                                   Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT14009;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                                                                                        a-----gggggggggcgccgctgccccggctgagcgcatggagcggt 178
                                                                                                                                                                                                                                                                                        TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
                                                                                                                                             80 geggeggetatacegtggaggtgageateaaegaetacetggatatetaetgeeeeaeet 139
                                                                                                                                                                                                                                                                                                                                    acatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagcgaggct
                                                                                                                                                                                                                                                                                                                                                                                                         AGTICCAGCGCTACAGCGCCTICTCTCTGGGCTACGAGTICCACGCCGGCCACGAGTACT
    Score 128.8; DB 17; Length 555;
                                                   Indels
            Score Learn,
Pred. No. 1.3e-15;
Wismatches 82;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTACATCTCCACGCCCACTCACAACCT
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12.4%;
ilarity 67.7%;
Conservative 0
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299 agiticeaactetteacecectiticectgggetitigagiteeggeetggeeaegaataet 358

AGTICCAGGGTACAGGGCCTICTCTCTGGGCTACGAGTICCACGCCGGCCACGAGTACT

456

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the chancement, stimulation, proliferation or growth of cells expressing the neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neural growth, they may be administered to a mammal to exert a trophic of fect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the oll or her elby a minitor level.
                                                                                                                                                                                                                    LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a murine LERK-6 polypeptide.
                                                                                                                                                  Murine LERK-6 polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 37-38; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US17772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0920440
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-243567/20.
P-PSDB; AAY06820.
                                                                         24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9910495-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1999.
AAX32761;
                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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Early inflammatory response; marker; antibody; therapy; induction; lipopolysaccharides; cytokines; Interleukin-2; IL-2; TNF; ss.

Location/Qualifiers

Homo sapiens

Ø ..691 /*tag=

74..128 /*tag= b 1458..1463 /*tag= c

polyA_signal

sig_peptide

Key

W09207094-A.

90US-0607741. 91WO-US07704

15-OCT-1991; 16-OCT-1990;

30-APR-1992

UNMI) UNIV MICHIGAN

Dixit VM;

AAQ24595 standard; cDNA to mRNA; 1438 BP

(first entry)

06-NOV-1992

AAQ24595;

B61 cDNA sequence.

359 actacatctctgccacacctcccaacct 386

516 ACTACATCTCCACGCCCACTCACAACCT

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Poly(A)+ mRNA isolated from human umbilical vein endothelial cells (HUVE) was treated with TNF cyclohexamide and used to construct a lambda gill cDNA library. The library was screened using radiolabelled cDNA fragments derived from the 5' end of B61 DNA. Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf + for sequencing. Clone B61.1 contained the entire OFR encoding a protein of 205 residues (24 kb). The B61 gene is involved in early inflammatory response and serves as a marker. It may be detected by probes or by antibody-based immunoassay of biological fluids such as plasma, CSF or urine. These assays make it possible to predict a worsening in a disease process and allow the quantitative assessment of the magnitude of the inflammatory response. This information will allow the earlier admin. Of appropriate therapy, thereby shortening the disease process and limiting the patient's exposure to anti-inflammatory/immunosuppressive therapy. B61 induction is rapid and profound, hence it is easily detectable. The B61 response is highly specific to proinflammatory stimuli, being only made by cells exposed to lipopolysaccharides or cytokines such as IL-2 and TNF and not growth factors or interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           λq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene prod. used as marker to detect inflammatory response detecting the B61 gene in biological fluids or by using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-167172/20.
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82; Indels 24; Gaps

DB 20; Length 555;

3e-15;

Score 128.8; D Pred. No. 1.3e-0; Mismatches

12.48; 67.78;

Best Local Similarity 67.7 Matches 222; Conservative

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Query Match

279 ACAACAGCICGGGGGGGGCCCCGGGGCGGGGGCCCGGAGGCGGGGGGAGAGCAGI 338

acatcctgtacatggtgaatggtgaagggccacgcctctgtgaccaccggcagcgaggct 238 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCCACAGCCCCATCAAGTTCTCGGAGA 455

396 179

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239

us-09-904-954-1.rng

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completed: September 28, 2002, 00:26:44
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WPI; 1994-160538/20.
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Job time:
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                                                                                                                                                                                                  ### TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCGCGCGCCCGCAC 433
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                                                          137 CCGCTGCTGCCCCAAGGGCCCCGGAGGGGCCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
                                                                      AGCTCCAACCAGCACCTGCGGCGAGAGGCCTACACCGTGCAGGTGAACGTGAACGACTAT 256
                                                                                                                                CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                                                                                                                                                                                   ....-gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310
                                                                                                                                                                                                                     311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370
                                            Gaps
                                                                                                       AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTTACAGCGCCTTCTCTCTGGGCTACGAG
                                                                                                                                                                                                                                                                        TTCCACGCCGGCCACGAGTACTACTACTTCTCCACGCCCACTCACAACCTGCACTGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        eck receptor; eck receptor binding protein; EBP; B61; cancer; inflammation; wound; cytokine; protein tyrosine kinase; PTK; phosphorylation; ds.
                                           24;
                          Length
                        Score 116.4; DB 13; Length
Pred. No. 3.1e-13;
0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welcher AA;
G; 295 T; 0 other;
                                                                                                                                                                                                                                                                                                                    TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parker VP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
74..691
/*tag= a
C; 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fox GM,
                                                                                                                                                                                                                                                                                                                                                                     AAQ63770 standard; DNA; 1480
Sequence 1438 BP; 358 A; 412
                       11.2%;
illarity 57.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93EP-0118469.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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09-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1995
                                           263;
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                                                                                                                                                                                                                                                                                                                                                                                                                         B61 gene.
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                        Query Match
Best Local 9
                                  Local
                                         Matches
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The N-terminal sequence of EBP isolated from the conditioned medium of the SK-BR-3 cell line was identical to the N-terminal amino acid sequence predicted from the expression of the B61 gene (Holzman et al., Mol. Cell Biol. 10, 5830 (1990); WO9207094).

CDNA encoding EBP having the N-terminal and sequenced and, as expected, found to be identical to the B61 gene. The EBP gene expressed in CHO cells resulted in at least two The EBP gene expraying different mol. Wts. C-terminal sequencing revealed only the sequence KRLAA-COOH which indicated a polypeptide of 150 amino acids (EBPI-150).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 CCCGGAGGCGGGCCAGAGCAGTACGTGCTACATGGTGAGCCGCAACGGCTACCGCACC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAACGGGCGCGCGCGCGCGCAC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttcaaagaaggacacagctactacatctccaaacccatccaccagcatgaagaccgc 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTCCAACCAGCACCTGCGGCGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----gagcagtacatactgtacctggtggagcatgaggagtaccagctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 1480;
                                                             treating cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1480 BP; 359 A; 421 C; 393 G; 307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 116.4; DB 15;
Pred. No. 3.1e-13;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAÇ 591
                                                         - useful for
                                                                                                                                                   Disclosure; Page 27-28; 41pp; English
                                                         receptor binding proteins ation, wounds, etc.
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Best Local Similarity 57.4%;
Matches 263; Conservative
                                                                                          inflammation, wounds,
P-PSDB; AAR53634
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Searched:

Database

Result ٠ يو Sequence:

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Sequence 1
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                      US-08-445-065-11

US-08-959-524-11

US-08-441-216-1

US-08-048-129-1

US-09-048-129-1

US-09-048-129-1

US-08-440-815-3

US-08-440-815-3

US-08-440-815-3

US-08-440-815-3

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US-08-453-341-3

US-08-453-38-74-3

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CLASSIFICATION NAMES. 05/00/210/124
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/16/132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/14/426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/19/745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE KATHYN A.
REGISTRATION NUMBER: 32/172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08240124
Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
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(206) 233-0644
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                   TELEPHONE:
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-920-440B-9

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US-08-455-001-3
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US-09-173-492-7
US-09-173-133-7
US-09-165-533-7
US-09-609-324A-1
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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us-09-904-954-1.rni

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ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08453943 Patent No. 5738844 GENERAL INFORMATION:
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                                                                                                                                                                                               1021 GTCTCGTTCCAAGATCC 1037
                                                                                                                                                                                                                         1021 GTCTCGTTCCAAGATCC 1037
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                       sig_peptide
83..139
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                                                               NAME/KEY: CDS
LOCATION: 83..799
FEATURE: NAME/KEY: sig_pepti
LOCATION: 83..139
FEATURE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L A2
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; LOCATION:
US-08-240-124-1
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APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR AFFLICATION DATE:

PRIOR AFFLICATION NUMBER: US 08/240,124

PELLING DATE: U9-NAY-1994

APPLICATION NUMBER: US 08/161,132

FILING DATE: 03-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/114,426

FILING DATE: 30-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/109,745

FILING DATE: 20-AUG-1993

ATORNEY/AGENT INFORMATION:

NAME: SEESE, KATHRYN A.

REGISTRATION NUMBER: 2814-C

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECHOME: (206) 587-0430

TELEFAX: (206) 233-0644
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CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC
TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: Apple System 7.1 Microsoft Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: US 08/161,132
FILING DATE:
APPLICATION DATE:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AGG-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AGG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: BECKNANN, M. P.
APPLICANT: BECKNANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT E
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSED: INMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
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THAT 1
HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/057,12
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/09057121
Patent No. 5969110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                1021 GTCTCGTTCCAAGATCC 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                  1021 GTCTCGTTCCAAGATCC 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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CLASSIFICATION:
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MOLECULE TYPE:
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                                                                                                                                                                                             Length 1037;
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Pred. No. 1.8e-194;
0; Mismatches 0;
                                                                                                                                                                                             100.0%;
100.0%;
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Best Local Similarity 100.
Matches 1037; Conservative
                                                                                                                              mat_peptide
140..796
                                                                                       sig_peptide
83..139
                                                             83..799
      IMMEDIATE SOURCE:
CLONE: hek-L A2
CLONE: hek-L A2
LOCATION: 83..799
FEATURE:
NAME/KEY: sig_pep
LOCATION: 83..139
                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-453-943-1
ANTI-SENSE:
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TGGAAGGAGCAGGGAGCCTTTTGGCCTCTCCAAGGGAAGCCTAGTGGGGCCTAGACCCCTCC
                                                                        TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZTE: 98101
COMBUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Apple Macintosh
OPENATING SYSTEM: Apple System 7.1
OPENATING SYSTEM: Mord for Apple, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/358,734
FILING DATE:
CLASSIPECATION STATE:
CLASSIPECATION:
PRIOR APPLICATION NUMBER: US/09/358,734
APPLICATION NUMBER: US/09/358,734
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A:
NAME: SEESE, KATHRYN A:
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 537-044
TELERA: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT
TITLE OF INVENTION: RECEPTOR HEK
WUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                           US-09-358-734-1
; Sequence 1, Application US/09358734
; Patent No. 6274117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                       1021 GTCTCGTTCCAAGATCC 1037
                                                                                                                                                                                        GICTCGTTCCAAGATCC 1037
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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CLONE: hek-L A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                    Ouery Match 100.0%; Score 1037; DB 2; Length 1037; Best Local Similarity 100.0%; Pred. No. 1.8e-194; Matches 1037; Conservative 0; Mismatches 0; Indels 0;
                                                                                    sig_peptide
83..139
                                                                                                                                mat_peptide
140..796
                                                       83..799
             hek-L A2
                        FEATURE:
NAME/KEY: CDS
LOCATION: 83..7
FEATURE:
NAME/KEY: $19_F
LOCATION: 83..1
FEATURE:
IMMEDIATE SOURCE:
CLONE: hek-L ?
                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-057-121-1
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APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 907.4; DB 1;
Pred. No. 3.6e-169;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                     3: Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                       Sequence 8, Application US/08299567
Patent No. 5747033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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96.3%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 96.3
Matches 939; Conservative
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US-08-299-567-8
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Pred. No. 1.8e-194;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 1037; Conservative
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140..796
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83..139
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NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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US-09-358-734-1
                                                                      NAME/KEY:
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APPLICANT: CERRETI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR FILING DATE: 1997-08-29
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-39
PRIOR FILING DATE: 1994-10-03
PRIOR FILING DATE: 1994-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09609324A Patent No. RE37582
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TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
NUMBER OF ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                   1.2e-21;
                                                                                                                                                                                                                                        14.6%; Score 151.8;
61.0%; Pred. No. 1.26
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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Matches 340; Conservative
                                                                                                                                  LOCATION: (1)..(639)
NAME/KEY: mat_peptide
LOCATION: (88)..(639)
US-09-609-324A-9
NUMBER OF SEQ ID NOS:
                 PatentIn
                                                                              ORGANISM: LERK-6
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-920-440B-9
                                SEQ ID NO 9
LENGTH: 642
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                                                                  TYPE: DNA
                                                                                                                                                                                                                                        Query Match
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Henry, Janis C. REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                       Sequence 9, Application US/09173492; Patent No. 6194172
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TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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11642
Signal Peptide
1-90
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ilarity 61.0%;
Conservative (
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                                 589 CACATCGCACTCCGGGG 605
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
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Best Local Simi
Matches 340;
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                                                                                                                     US-09-173-492-9
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STATE:
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0; Mismatches 172; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
COMPUTER: Spalem 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 29-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 2826-B
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: NOCHOLE CALLOR SEG ID STORE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: NOCHOLE CALLOR SEG ID STORE CHARACTERISTICS:
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LENGTH: 642 base pairs
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61.0%; Pred. No. 1.2
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Signal Peptide
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US-08-920-440B-9
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                                                                                                                                                                                                                                                                                          COMPUTE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,492
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Pred. No. 1.2e-21;
0; Mismatches 172;
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GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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GCAGGTGAACGTGAACGTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT
                                                                                                                     355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG
                                                          295 GGCCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACATGGT
               183 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCGCACTAT----
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/09/173,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: US,08/920,440
FILING DATE: 29-40G-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Jan1s C.
REGISTATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09173133 Patent No. 6232447
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TELEFAX: (206) 233-0644
INPORMATION FOR SED ID NO: 9: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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ANTI-SENSE: NC
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: W
COUNTRY:
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73 GGCTCCGGGGATGGCGGCGCGCTCCGCTGCTGCTGCTGCTGCTCGTGCCGGTGCCGGT 132
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                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                           3 GGGCCCGCGCGCAGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCCGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                         123 GAACCGCAGCAACCCCAGGTTCCACGCAGGCGCGGGGGACGACGGCGGGGGGGTACACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 GGGCCCCGGGGCGGGCCGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG----GGCTTCAAGCGCTGGGAGTG
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                                                                                                                                                                   45;
                                                                                                                                Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Flangan, John G.
APPLICANT: Flangan, John G.
APPLICANT: Cheng, Hwal-Jong
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                   Indels
                                                                                                                                  .,
                                                                                                                               Score 151.8; DB 4;
Pred. No. 1.2e-21;
0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08455001
Patent No. 5795734
   CDS
11642
Signal Peptide
1-90
                                                                                                                               14.6%;
llarity 61.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 CACATCGCACTCCGGGG 605
                                                                                                                               Query Match
Best Local Similarity
Matches 340; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
; LOCATION:
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; LOCATION:
US-09-173-133-9
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US-08-455-001-3
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109 GTGCAACCGGCCGCACGCCCCCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GGACCGCTACGCCGTCTATTGGAACCGCAGCAACCCCAGGTTCCACCGCGGGGATTACAC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 GGTCAACTACGAGGGCCACGCGTCCTGCGACCACCGGCAGAAGGGCTTCAAACGTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 783;
                                                       TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 149.2; DB 5;
Pred. No. 4e-21;
0; Mismatches 133;
                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGRNT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE:
 Sequence 3, Application PC/TUS9511869
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ilarity 63.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686..783
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                       GENERAL INFORMATION
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LOCATION:
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LOCATION:
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LOCATION:
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Best Local Simi
Matches 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
PCT-US95-11869-3
                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%; Score 149.2; DB 63.3%; Pred. No. 4e-21;
                                                                                                                                                    HMI-011CP2
                                       UMBER: US/08/455,001
31 MAY 1995
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNDBER: 36,709
REFRENCE/DOCKET UNDBER:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                 LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 63.3
Matches 276; Conservative
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86..148
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LOCATION:
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-455-001-3
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PCT-US95-11869-3
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; NAME/KEY:
; LOCATION:
PCT-US95-11869-1
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FEATURE:
NAME/KEY:
LOCATION:
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445 CACCCCCTTCTTTGGGCTTCGAGTTCCGTCCCGGCCACGAGTATTACTACATCTCTGC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 CGGGGGGGGGGGGGGGGGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGCTGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 CGCTGCTGCTGCTGCTGCCGCTGCGTGCGCAACGAGGACCCGGCCCGGGCCAACG 352
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                                                                                                                                        Sequence 1, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.4%; Score 149.2; DB 1; Length 1
Best Local Similarity 62.6%; Pred. No. 4.5e-21;
Matches 322; Conservative 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
RECISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
INFORMATION: POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
                                                   529 GCCCACTCACAACCTG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
255..324
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'UTR
1..264
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STATE: MA
COUNTRY: USA
TO: 02109
                                                                                                                                                                                                                                                                                                                                                    USA
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LOCATION:
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-455-001-1
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                                                                                                             RESULT 12
US-08-455-001-1
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413 GTGATGGGGGGGTATACCGTGGGGGGTGAGCATCAACGACTACCTGGATATCTACTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                        632 CAGAGAAGTTCCAACTCTTCACCCCCTTTTCCCTGGGCTTTGAGTTCCGGCCTGGCCACG
                                                        219 -----GAGAGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC
                                                                                                                                                                                                                                                                                                     392 --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCT
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TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AGTACTACATCTCCACGCCCACTCACAACCT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-0595-11869-1; Sequence 1, Application PC/TUS9511869; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7709
REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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255..324
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265..891
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126 TAGCAACCCCAGGTTTCAGGTGAGCGCTGTGGGTGATGGCGGCGTATACCGTGGAGGT 185
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                                                                                                                                                                                                                                                                                                                                                       139 GCTGCTGGCCCAAGGGCCCCGGAGGGCCCTGGGAAACCGGCATGCGGTGTACTGGAACAG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 CICTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCA 537
                                                                                                                                                                                                                                                                                                                                                                                    99 CICCAACCAGCACCTGCGGC------GAGAGGGCTACACCGTGCAGGT
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Pred. No. 7.7e-21;
0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A7772
CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR PLING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/538,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09609324A Patent No. RE37582
            TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1615 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          14.38;
62.68;
                                                                                                                                                                                                                                                                                         Query Match 14.3
Best Local Similarity 62.6
Matches 304; Conservative
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10..69
                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-308-814-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTGGGCTACGAGTTCCACGCCGGCCACG
                                                           44;
                         Length 1809;
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APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwal Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                           Score 149.2; DB 5; Length :
Pred. No. 4.5e-21;
0; Mismatches 148; Indels
                                                                                                                                                                                                              171 GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC--
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,814
FILING DATE: 19-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: HMI-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                           14.4%;
62.6%;
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                                                         Conservative
                                           Similarity
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                                                         Matches 322;
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US-08-308-814-1
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STATE:
                           Query Match
                                           Best Local
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Gaps

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                                                                                                                                                                                                                                                                                                                                          at-----ggggcgccgctgccgccggcgagcgatggagcact 125
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                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 27, 2002, 22:42:54 Job time: 8650 sec
PRIOR FILING DATE: 1995-10-03
PRIOR APPLICATION NUMBER: 08/318,393
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 314
TYPE: DNA
ORGANISM: LERK-6
                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(313)
US-09-609-324A-7
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Run on:

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September 27, 2002, 21:26:30 ; Search time 3673.16 Seconds (without alignments) 6107.926 Million cell updates/sec
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1037
1 GGATCTTGGAACGAGACGAC......GTCGTCTCGTTCCAAGATCC 1037
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/cgn2_6/ptodata/2/pna/US6004_COMB.seq:
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	7,	1,	1,	Seguence 1, Appli	e 10	Т		Н	ω	Sequence 8, Appli	e 1158	53,	98,		182,	241,	241,		27387	2819		27387,	2819	Sequence 577, App	622,	70, App	1031	3231,		600,	Sequence 8616, Ap
QI	-US94-0928	2-03-304-32	-08-109	US-08-161-132-1	-60-172-373	-60-278-258	US-09-440-302A-838	9-733-756	US-08-229-402-8	-327-423-8	-03-698-010-1	-09-948-941	-09-948-941-9	7-618	-09-221-481	US-09-440-302-241	US-09-440-302A-241	-09-880-093-64	US-09-235-076-27387	9-289-768	$^{\circ}$	-223-273	US-09-939-397-28196	-09-948-941	US-09-948-941-622	-60-212-656-70	-09-699-997-10	-60-169-868	-09-699-997-31	-60-212-656-600	US-09-534-853-8616
DB	Н	34					18												16												
% Query Match Length DB	1037	1037	1037	1037	1761	1761	987	1743	1070	1070	818	717	717	421	392	392	391	497	442	442	442	442	442	11602	11603	22453	999	627	468	2332	339
% Query Match	100.0	100.0	99.7	99.7	95.4	95.4	95.2	88.5	7			69.1	69.1	39.7	37.8	37.8			33.8				33.8	33.4	33.4	33.4	33.3	32.4	32.2	32.2	29.8
Score	1037	1037	1033.8	1033.8	988.8	988.8	286	917.8	907.4	907.4	773	717	717	411.8	392	392	391	351.2	350.8	350.8	350.8	350.8	350.8	46	346.8	346.8	345.8	335.8	334	33	308.8
Result No.	-	~	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	c 26	27	c 28	29	30	31

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100.0%; Pred. No. 5.1e-160;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1037; Conservative
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140..796
                   83..799
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
PCT-US94-09282-1
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09282
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY,AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION UMBER: 32,172
REGISTRATION UMBER: 32,172
B US-09-404-549-2399
B US-09-414-5434-239
B US-09-474-434-253
B US-09-474-434-253
C US-60-173-686-253
C US-60-173-686-715
C US-60-173-686-7189
C US-60-194-508-7189
C US-09-598-68650
US-09-59-68650
US-08-104-5077-756
US-08-104-5077-756
                                                                                                                                                                                                            US-09-605-784A-440
US-08-222-075-5
                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9409282
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BI
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
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TELECOMMUNICATION INFORMATION:
TELEPRAN: (206) 537-044
TELERAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRARCTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET CITY: SEATILE
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CLONE: hek-L A2
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 841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCTTC 900
                                       901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCCTTACCCTTCC
                                                                                                                                                                                                                                ARE INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
SNPTICATION DATA:
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: <UNKNOWN>
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/240,124
FILING DATE: CURKNOWD>
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-A0(5-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: SEESE, KATHRYN A.
REGISTRATION UNBER: 23.172
REPERENCE, DOCKET NUBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPRAN: (206) 587-0430
TELEPRAN: (206) 233-0644
TELEX: 756822
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SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                     Sequence 1, Application US/09904954 GENERAL INFORMATION:
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                                                                                                                                              Indels
                                                                                                          100.0%; Score 1037; DB 34; 100.0%; Pred. No. 5.1e-160;
                                                                                                                                              0; Mismatches
                                  ä
NAME/KEY: mat_peptide
LOCATION: 140..796
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                             Best Local Similarity 100. Matches 1037; Conservative
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961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
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  111 GCCCGTGCCGCTGCTGCTGCTGCTGCCCCAAGGCCCCGGAGGGGGCGCTGGGAAACCGGCAAA
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US-08-161-132-1
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                                                                                                                               US-08-109-745-1
Sequence 1, Application US/08109745
GENERAL INFORMATION:
APPLICANT: BECKANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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COMPUTER: APPLE MACINICOSH

COMBUTER: APPLE MACINICOSH

COMBUTER: APPLE MACINICOSH

COMBUTER: APPLE MACINICOSH

SOFTWARE: MACTOSOFT WORD, VERSION 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/109,745

FILING DATE: 20-AUG-1993

CLASSIFICATION: 530

ATORNEY/AGENT INFORMATION:

NAME: SEESE, KATHRYN A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2814

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELETAX: (206) 233-0644

TELETAX: 756822

INFORMATION FOR SEC ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENTH: 1037 base pairs
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Pred. No. 1.7e-159;
0; Mismatches 2;
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Best Local Similarity 99.8%;
Matches 1035; Conservative (
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                                                                     1021 GTCTCGTTCCAAGATCC 1037
                                                    1021 GTCTCGTTCCAAGATCC 1037
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83..139
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140..796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
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HYPOTHETICAL:
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FEATURE:
NAME/KEY: C
LOCATION: E
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LOCATION:
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US-08-109-745-1
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909 900 999 999 720

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Sequence 10727, Application US/60172373
GUNERAL INFORMATION:
APPLICANT: MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0006 p
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                            361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC
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                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,132
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Pred. No. 1.7e-159;
0; Mismatches 2;
           APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETT, DOUGLAS P.
APPLICANT: CERRETT, DOUGLAS P.
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
ADDRESSE: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435

RELOR APPLICATION DATA:
APPLICATION NUMBER: 05 9/114,426
FILING DATE: 30-NG-1993
PRIOR APPLICATION NUMBER: 05 08/109,745
FILING DATE: 20-NG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHENN A.
REFERENCE/DOCKET NUMBER: 2814-B
TELEPHONE: (206) 233-0644
TELEPHONE: (206) 233-0644
TELEFAX: (206) 233-0644
TELEFAX: 756822
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      3: IMMUNEX CORPORATION 51 UNIVERSITY STREET
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99.8%;
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TYPE: nucleic acid
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Matches 1035; Conservative
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83..139
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                                                                                                                                 CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
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GENERAL INFORMATION:
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STRANDEDNESS:
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LOCATION:
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LOCATION:
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US-08-161-132-1
                                                                                                                    STREET:
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Pred. No. 3.7e-152,
0; Mismatches 2,
                                                                                  CAAGCACGGGACAGCCATGGGTCCCGAGCAG 1017
                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 406106.
US-60-278-258-13410
                                                                                           95.4%;
                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 99.8
Matches 990; Conservative
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                      US-60-278-258-13410
                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                  986
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                                                                                                                            Length 1761;
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                                                                                                                             DB 56;
                                                                                                                            Score 988.8; DB 56
Pred. No. 3.7e-152;
0; Mismatches 2;
                                                                          ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 406106.1
US-60-172-373-10727
CURRENT APPLICATION NUMBER: US/60/172,373
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772
SOFWARE: PERL PROGram
SEQ ID NO 10727
                                                                                                                            95.4%;
99.8%;
                                                                                                                                      Best Local Similarity 99.8
Matches 990; Conservative
                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                             Duery Match
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Sequence 13410, Application US/60278258

Sequence 13410, Application US/60278258

GENERAL INFORMATION:
APPLICANT: Macronald
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Us
TITLE OF INVENTION: Polymorphisms Identified Thereby
FILE REFERENCE: CX-0010-1 Profile Sequence Databases, and Single Nucleotide
FILE REFERENCE: CX-0010-1 Profile Sequence Databases, and Single Nucleotide
CURRENT APPLICATION UNDBER: US/60/278,258
CURRENT FILING DATE: 2001-3-23
NUMBER OF SEQ ID NOS: 17730
SOFTWARE: PERL PROGRAM
SEQ ID NO 13410
LENGTH: 1761
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                     TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC
                                                                                      926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC
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pplication US/09733756
MATION:
MATION:
G1sh, Kurt C.
Milson, Keith E.
MATION: METHODS OF DIAGNOSING COLORECTAL CANCER AND/OR BREAST CA
ENTION: NOVEL METHODS OF SCREENING FOR COLORECTAL CANCER
ENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
ENTION: CANCER MODULATORS
CER: A-64347DABJJJD
CCATION NUMBER: US/09/733,756
NG DATE: 2000-12-08 AGGGAAGCCTAGTGGGCCTAGACCCCTCCCATGGCTAGAAGTGGGGCCTGC 925 CATCTGTGTCGCCCCCTCTACCCCTTCCCCCCAGGGGGCACTGTAGTGGAC 985 GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCGCACACGCCCCATCAAG CAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC CGGGGACAGCCATGGGTCCCG 1012

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GGGCTCAGTCGGGGGGGGGGGGGGGGGGGGGGGGGATGGCGGGGGGCGCTGCTG 103
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781 agcctagtgggcctagacccctcctcccatggctagaagtggggcctgcaccatacatct
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Pred. No. 7.5e-139;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                   APPLICANT: Davis, et al.
TITLE OF INVENTION: EPH Family Ligands
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-NOV-1993
PRIOR APPLICATION NUMBER: US 07/736,559
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 336
PRIOR APPLICATION NUMBER: US 08/222,075
FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,402
FILING DATE: 12-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              Sequence 8, Application US/08229402 GENERAL INFORMATION:
                                                                                                                                                 997 ACAGCCATGGGTCCCGAGCAG 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kempler Ph.D., Gail M. REGISTRATION NUMBER: 32,143
                                                                                                                                                                   901 acagecatgggtecegggegg 921
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TELEPHONE: 914-345-7400
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96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1070 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 96.3
Matches 939; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          914-347-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10591
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                                                                                                                                                                                                                                                                                                                   Score 917.8; DB 29
Pred. No. 1.5e-140;
0; Mismatches 2;
             PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 09/493,444
PRIOR APPLICATION NUMBER: US 09/453,850
PRIOR APPLICATION NUMBER: US 09/453,850
PRIOR PILING DATE: 1999-12-02
PRIOR PRICATION NUMBER: PCT/US 00/07044
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
 APPLICATION NUMBER: US 09/525,993
                                                                                                                                                                                                                                                                                                                   88.5%;
99.8%;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.8
Matches 919; Conservative
                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-733-756-1
                                                                                                                                                                                                          LENGTH: 1743
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                      SEQ ID NO 1
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Best Local Similarity 96.3
Matches 939; Conservative
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                                          TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG
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                                  GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC
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GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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US-08-327-423-8
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Score 907.4; DB 7; Pred. No. 7.5e-139; 0; Mismatches 24;

87.5%; 96.3%;

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#1.30
                                                                                                                                             Version
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,423
FILING DATE: 21-COT-1994
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 08/299,567
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gall M.
REGISTRATION NUMBER: 32,143
                                  ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RI
TELECOMMUNICATION INFORMATION
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-327-423-8
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LENGTH: 1070 base pairs
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
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385

445 465 525 565 585 625 645 685

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Sequence 53, Application US/09948941

GENERAL INFORMATION:
APPLICANT: VENYER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO00788
CURRENT EPLING DATE: 2010-09-10
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 12618
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 717
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gcccaagggcccggagggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 225
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                                                                                       TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGC
                                                                                                                                              GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC
                              CAGCACCTGCGGCGAGAGGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT
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Best Local Similarity
Matches 717; Conserv
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US-09-948-941-53
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US-09-948-941-53
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                                                          CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAAGAACCCTCAGGTGCCCAAG
 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC
                          GCCTCCACATCGCACTCCGGGGGGGAAAGCCGGTCCCCCACTCCCCCCAGTTCACCATGGGC
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GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREPOR
FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 1200-10-27
PRIOR APPLICATION NUMBER: 60/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF FSQ ID NOS: 15684
SOFTWARE: FastESQ for Windows Version 4.0
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100.0%; Pred. No. 6.9e-117;
tive 0; Mismatches 0;
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; LOCATION: (1)...(818)
; OTHER INFORMATION: n = A,T,C or G
US-09-698-010-11586
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Best Local Similarity 100.
Matches 773; Conservative
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LOCATION: (1)...(421)

COTHER INFORMATION: n =

US-09-287-618-6642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES;
FILE REFERENCE: CLOOO788
CURRENT APPLICATION NUMBER: US/09/948,941
CURRENT APPLICATION NUMBER: 60/231,328
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR APPLICATION NUMBER: 60/231,328
NUMBER OF SEQ ID NOS: 12618
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
LENGTH: 717
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llarity 100.0%; Pred. No. 9.8e-108;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 717; Conserv
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CRGANISM: Human
US-09-948-941-98
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                                                          AACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGAT
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-768
CURRENT APPLICATION NUMBER: US/09/287,618
CURRENT APPLICATION DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 35865
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 7.3e-58;
); Mismatches 3;
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Pred. No. 1.3e-54;
0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-221-481-182
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US-09-221-481-182
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-440-305B-838
US-09-440-305B-221
US-09-918-995-27387
US-09-055-375B-1095
US-09-919-039-161
PCT-US02-13644-14
US-09-055-375B-1504
US-09-442-384B-743
US-09-440-302B-837
US-09-440-302B-837
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US-10-171-581-190
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•		PEBULT PCT-US02-25766-6624 Sequence 6624, Application PC/TUS02 GENERAL INFORMATION: APPLICANT: GENE LOGIC, INC. APPLICANT: FAULK, Ronald APPLICANT: FAULK, Ronald APPLICANT: SASAI, Hitoshi APPLICANT: SASAI, Hitoshi APPLICANT: WAGA, Iwao APPLICANT: WAGA, Iwao APPLICANT: WAGA, Iwao APPLICANT: WAGA, Iwao CURRENT: WAGA, Iwao FILE REFERENCE: 44921-5068-WO CURRENT FILING DATE: 2002-08-14 PRIOR FILING DATE: 2002-08-14 PRIOR FILING DATE: 2001-08-14 NUMBER OF SEQ ID NOS: 13946 SOFTWARE: PATCATION NUMBER: US 60/31 PRIOR FILING DATE: 201 SOFTWARE: PATCATION NUMBER: US 60/31 PRIOR FILING DATE: 201-08-14 CURRENT FILING DATE: 2002-08-14 CURRENT FILING DATE: 2002-08-14 PRIOR FILING DATE: 2002-08-14 CURRENT	99 90 90 90

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902 181 GGGGCAGAGCAGTACTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc

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                                         AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 987
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Length 987;

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Score 987;

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llarity 100.0%; Pred. No. 3.3e-56;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                             APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP13
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 2216
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-292
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 392; Conserv
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                                                                                                                                                                                                                                             1.6e-154;
                                                                                                                                                                                                                           95.2%; Scor.
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                     Score 987; DB
                             APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-03-31
                                                                                                                           NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
         Sequence 838, Application US/09440302B GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-440-302B-838
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 987; Conserv
                                                                                                                                                  SEQ ID NO 838
LENGTH: 987
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                                                                                                                                                                                                                                                                                                                                      870 CAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCA
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                                                                                                                                                                                                                              Score 350.8; DB 5
Pred. No. 2.1e-49;
0; Mismatches 24
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Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Nucleic Acid Arrays
TITLE FERENERNCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SEQ ID NO 1095
SEQ ID NO 1095
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                                                                                                                           ; LOCATION: (1)...(442)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27387
                                                                                                                                                                                                                                33.8%;
93.8%;
                                                                                                                                                                                                                            Query Match 33.8
Best Local Similarity 93.8
Matches 364; Conservative
                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(442)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 326; Conserv
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  SEQ ID NO 27387
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERBACE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTESQ FOR WINDOWS VERSION 3.0
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Best Local Similarity 100.0%; Pred. No. 4.9e-56;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                        APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILING DATE: 1999-11-17
PRIOR PELING DATE: 1998-11-17
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
361 aggatgaaggtgttcgtctgctgcgcctccac 392
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                                                                         US-09-440-302B-241; Sequence 241, Application US/09440302B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-918-995-27387
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LENGTH: 391
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Length 1594;

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DEFICIONT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL PROGram

SEQ ID NO 161

LENGTH: 1557
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                                                                                                                                                                      260 gcccacacta------ggggcgccgctgcccggctgagcgca
                                                                                                                                                                                                                 219 ------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATTTACT
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Pred. No. 7.2e-11;
0; Mismatches 245; Indels
                            168 TGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC--
                                                                                                                                                                                                                                                                                                                                                                             ACGAGTACTACATCTCCACGCCCACTCACAACCT 543
                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 405844.22
US-09-919-039-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 161, Application US/09919039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.3%;
Best Local Similarity 53.4%;
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-919-039-161
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APPLICANT: Chied, Kenneth
APPLICANT: Chied, Kenneth
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: NOn-viral vesicle vector for cardiac specific gene delivery
FILE REFERENCE: 6627-Pal198
CURRENT APPLICATION NUMBER: PCT/USO2/13644
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: 60/287,423
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                       317 CCCGGAGGCGGGCAGAGCAGTACGTGTTACATGGTGAGCCGCAACGGCTACCGCACC 376
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                                                                                                   ....-tggagcagtacatactgtacctggtggagcatgaggagtaccagctgt 352
                                                                                                                                  378 GCAACGCC----AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACA 434
                                                                                                                                                                    353 gecagececagtecaaggaceaagteegetggeagtgeaaceggeecagtgeeaageatg 412
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Gaps
                 TCCACGCCGGCCACGAGTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGT
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                                                                 CCGGAGGCGGGCGAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCT
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Pred. No. 9.1e-11;
0; Mismatches 171;
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FORTHORNATION PC/TUS0213644
GENERAL INFORMATION:
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Best Local Similarity 57.4%;
Matches 263; Conservative
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ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: homo sapiens
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CORGANISM: Homo Sapiens
US-09-440-302B-837
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Best Local Similarity
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371 ggcccggagagctgtctgagaagttccagcgcttcacactttcaccctgggcaaggag 430
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                                    TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG
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Pred. No. 9.1e-11;
0; Mismatches 171;
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GENERAL INFORMATION:
APPLICANT: Chenchik. Alex
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILLNG DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1504
LENGTH: 1480
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Sequence 743, Application US/09442384B
GENERAL INFORMATION:
PAPPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey
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Best Local Similarity 57.4%;
Matches 263; Conservative (
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; ORGANISM: Homo sapiens
US-09-053-375B-1504
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Pred. No. 9.1e-11;
0; Mismatches 171;
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TITLE OF INVENTION: Hematology/Immunology Array FILE REFERENCE: CLON-006CIP15
CURRENT APPLICATION NUMBER: US/09/442,384B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 830
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 743
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TILLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT EDLING DATE: 1999-11-17
PRIOR PELICATION NUMBER: 09/053,375
PRIOR PLING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 9.1e-11;
); Mismatches 171;
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; ORGANISM: Homo sapiens
US-10-136-819-14
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Matches 263;
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                                                                      AGCTCCAACCAGCACCTGCGGCGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
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  Length 1480;
             Pred. No. 9.1e-11;
0; Mismatches 171; Indels
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APPLICAMT: BIRNBAUM, DANIEL
APPLICAMT: NOUFEN, CATHERINE
APPLICAMT: NOUFEN, CATHERINE
APPLICAMT: NOUFEN, CATHERINE
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ITILE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY
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CURRENT APPLICATION NUMBER: US,10/07,926A
CURRENT APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 27
LENGTH: 1480
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 DB 5;
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Pred. No. 9.1e-11;
0; Mismatches 171;
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 Score 116.4;
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US-10-007-926A-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 227, Application US/10007926A; GENERAL INFORMATION: APPLICANT: BERTUCCI, FRANCOIS
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sal Similarity 57.4%;
263; Conservative
              Best Local Similarity 57.4
Matches 263; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 263; Conserva
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Query Match
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NSGUENCE 14. Application US/10136819
Sequence 14. Application US/10136819
Sequence 14. Application US/10136819
Sequence 14. Application Sequence 15. Expression Sequence 15. Sequenc 3 434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTCACACGCCTTCTCTGGGCTACGAG 493 371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376 ------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310 TGCAACGCCAG----CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433 317 CCCGGAGGCGGGGCAGAGCAGTACGTGTTACATGGTGAGCCGCAACGGCTACCGCACC 376 TTCCACGCCGGCCACGAGTACTACTACTACTCTCCACGCCCCACTCACAACCTGCACAGG 553 CCGCTGCTGGCCCCAAGGGCCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196 cetetettgggtetgtgetgeagtetggeegetgetgategeeacacegtettetggaae 151 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211 377 TGCAACGCCAG----CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac Length 1480;

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APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Anohan, John
APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Gatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/335,936
NUMBER OF SEQ ID NOS: 238
SOFID NO 49
LENGTH: 1480
TYPE: DNA
CREANISM: Homo sapiens
US-10-171-311-49
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                                                                         494 TICCACGCCGGCCACGAGIACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 CCGCTGCTGCCCCAAGGCCCCGGAGGGCCCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
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                                                                                                                                                                   554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
                                                                                                                                                                                                                                            RESULT 15
US-10-171-311-49
Sequence 49, Application US/10171311
GENERAL INFORMATION:
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APPLICANT: Chen, Yan
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Search completed: September 28, 2002, 01:35:23 Job time: 12723 sec

us-09-904-954-1.rnpn

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BE663141 126832 MA BG69896 602703313 BB833304 BB833304 BF394888 UI-R-CA0-BB30682 BB830682 AL26332 TELRAGOON AA399416 mp12q10.T AL565095 AL565095 AA389014 mp13c10.T AK020438 Mus muscu AL212116 TETRAGOON BE648416 UI-M-BH2. AL653020 AL563020 AA170896 ms49f67.T AL630156 AL661297 AL553020 AL563020 BA17326 C06699 MA BU073054 BJ010542 BU075270 BJ01542 BU075270 BJ01542 BU075270 BJ01542 BU075270 BJ016428

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198 187.4 180.6 177 165.4 165.2 1153.8 1151.2 146.6 143.8

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BJ074739 BJ074739 BJ065530 BJ0764739 BJ096950 BJ096950 BJ094859 BJ094859 BB643986 BB643986

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.		
OM nucleic - nucleic search, using sw model		
Run on: September 27, 2002, 20:13:14 ; Search time 2180.79 Seconds (without alignments) 6418.015 Million cell updates/sec	9 Seconds 1 updates/sec	
Title: US-09-904-954-1 Perfect score: 1037 Sequence: 1 GGATCTTGGAACGACGACGTCGTCTCGTTCCAAGATCC 1037	ICC 1037	
Scoring table: IDENTITY_NUC Gapext 1.0		
Searched: 13736207 seqs, 6748477542 residues		
Total number of hits satisfying chosen parameters: 27472414		
Minimum DB seq length: 0 Maximum DB seq length: 2000000000		
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ALIGNMENTS

	1030 bp mRNA linear EST 13-FEB-2001	AL533153 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0D		AL533153.1 GI:12796646	EST.		Homo sapiens	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1030)	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope	Genoscope - Centre National de Sequencage	BP 191 91006 EVRY cedex - France	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	Location/Qualifiers		/organism="Homo sapiens"	/db_xref="taxon:9606" ,	/clone="CSODNO03YL19"	/clone lib="LTI FL015 Brn1"	/sex="male"	/tissue_type="Adult brain"	/note="Vector: pcMvSPORT 6; Site_1: Not1; 1st strand cDNA	was primed with a NotI-oligo(dT) primer. Five prime end	enriched, double-stranded cDNA was digested with Not I and	cloned into the Not I and Eco RV sites of the pCMVSPORT 6	vector. Library was constructed by Life Technologies.	Contact : Feng Liang Life Technologies, a division of	Invitrogen 9800 Medical Center Drive Rockville, Maryland	COSO, USA FAX: (1) SU OLO OS/A EMAIL :	illangellieteth.com okb : http://fulllength.invitrogen.com"	183 a	בין אייני אינין אינין
KESULT I	AL533153	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT				FEATURES	· source																RASE COTINT	ORIGIN

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss:* em_gss_hum:*

gb_est2: gb_htc:*

em_esthum:*
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em_estov:*
em_estol:*
em_estc:*
gb_est1:*

em_estba:*

Database

em_gss_inv:*

Description

DB

Query Match Length I

Score

Result ٠ يو BASE COUNT ORIGIN

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BF953157 CM3-NN118
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804 bp mRNA linear EST 23-JAN-2001
Homo sapiens cDNA clone IMAGE:4397263 5',
                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/note="lorgan: small intestine; Vector: pCMV-SPORT6;
Site_1: Not!; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
the constructed by Life
256 c 265 g 133 t a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM10097 row: i column: 08
High quality sequence stop: 766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 GCCCAAGGGCCCGGAGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC
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Pred. No. 8.5e-96; .
0; Mismatches 34; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TWAGE.4397263"
/clone_lib="NIH_MGC_88"
                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                       BF983120.1 GI:12386017
                      BF983120
602305829F1 NIH_MGC_88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.6%;
Best Local Similarity 94.6%;
Matches 749; Conservative (
                                               mRNA sequence.
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                                                            CCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGGCGGGGCCGGGGCCCGGAGGCGGGGCAA
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 Length 1030;
                       12; Indels
6
Score 901; DB 9;
Pred. No. 2e-136;
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86.9%;
98.0%;
                       Conservative
            Similarity
                       963;
 Query Match
            Local
                       Matches
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/lab_host="neuroblastoma cells"
/lab_host="neuroblastoma cells"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWVSDORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies. a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
          CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT
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/sex="male"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 902)
1 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 2.6e-90;
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AL546822 LTI_NFL006_PL2 Homo sapiens CDN prime, mRNA sequence.
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/db_xref="taxon:9606"
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/clone=="cosbloids/riza"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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tive 8; Mismatches 37
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/note="Organ: nervous_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A min: library was made by cloning products derived from ORSTSE PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under low stringency conditions.

144 c 162 g 96 t
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1 (bases 1 to 496)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2704022

Fax: +55-11-2707001

Email: asinpson@ludwig.org.br

Fax: 455-11-2707001

Email: saippson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=CM3&t2=CM3-NN1187-11100-478-aso&&&=2000-11-11&t4=1)

Seq primer: puc 18 forward: 19

High quality sequence strop: 495.
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                                                                                                                                                                                                                                                                                                                                          496 bp mRNA linear EST 22-JAN-200:
CM3-NN1187-111100-478-a06 NN1187 Homo sapiens CDNA, mRNA sequence.
BF953157
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                          AACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCCTCC-ACATCGCA 597
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1187"
/dev_stage="Adult"
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1 (Dases 1 to 884)

2 NIH-MGC http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Unpublished (1999)

2 Contact: Robert Stransberg, Ph.D.

2 Contact: Robert Stransberg, Ph.D.

2 Contact: Robert Stransberg, Ph.D.

3 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

3 Contact: Robert Stransberg, Ph.D.

4 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

5 Contact: Robert Stransberg, Ph.D.

5 Contact: Robert Stransberg, Ph.D.

6 Contact: Robert Stransberg, Ph.D.

7 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

6 Contact: Robert Stransberg, Ph.D.

7 Contact: Robert Stransberg, Ph.D.

7 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

7 Contact: Robert Stransberg, Ph.D.

8 Contact: Robert Stransberg, Ph.D.

8 Contact: Robert Stransberg, Ph.D.

8 Plate: LAMI0725 row: 1 Column: 01

8 High quality sequence stop: 587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG705182 884 bp mRNA linear EST 07-MAY-2001 602688106F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820496 5',
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/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
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BG705182.1 GI:13979264
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Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." 338 c 289 g 105 t
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0; Mismatches 96;
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                                             BASE COUNT
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AW786993
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TACCCCTTCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCC 1010
                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
BG743158.1 GI:14053811
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Best Local Similarity 99.5%;
Matches 365; Conservative C
                                                                                                                                                                                                      Homo sapiens
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                                                                                  Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980994.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for
                                                         Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
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                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 535)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
                                                                                                                                                       EST discovery in swine Unpublished (2000) Contact: Smith TPL USDA, ARS, US Weat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 409; DB 9;
94.4%; Pred. No. 6.4e-57;
ive 0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 44 row: E column: 17
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .535
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FORWARD: AGGAAACAGCTATGACCAT
 GI:7843769
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/uZ bp mRNA linear EST 15-MAY-2001
MRNA sequence.
BG743158
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/db_xref="taxon:9606"
/clone="ImAGE:4779506"
/clone=lib="NCI_CGAP_Skn3"
/lab_host="HHI0B (T1 phage-resistant)"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs:remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIOGIS row: p column: 03
High quality sequence stop: 702.
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.4e-49;
0; Mismatches 2; Indels
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CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTG
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/db_xref="taxon:9606"
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/clone="InAGE:4667314"
/clone="InAGE:4667314"
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/clone="Organ: kidney; Vector: pDNR-LIB (clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
/clone="Organ: kidney; Vector: pDNR-LIB (clontech); Site_1: Sfil (ggccgctcggcc);
/clone="Inage:4667"
/clone="I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 848)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

IAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM9G row: e column: 11

High quality sequence stop: 511.

RES 1. AAR
                                                                                                                                                                                                                                                                                  BF542148 848 bp mRNA linear EST 11-DEC-2000 602068243F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067314 5',
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301 TACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCC 360
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89.0%; Pred. No. 7.4e
tive 0; Mismatches
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BF542148.1 GI:11629529
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462; Conservative
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                                                             1011 CGAGCAG 1017
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Best Local S:
Matches 462
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, AL628407 AGC-gastrula Silurana tropicalis cDNA clone TGas008p08 5', /db_xref="taxon:8364"
/clone="TGas008p08"
/clone=lib="xGc-gastrula"
/dev_stage="gastrula" (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; 130 GCTGCTGCTGCTGCTGGCCCAAGGGCCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTA 189 924 401 864 Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers 0; Mismatches 124; Indels 24; Gaps Xenopodinae; Silurana.

1 (bases 1 to 552)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001)

Contact: Huckle E. 806 CCCCTCCCCTGGGGGGGGGAGATGGGGGGGGCTTGGAAGGAGCAGGA-GCCTTTGGC 282 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGGGGGACCAGCCCCAAACGGGAACACCTG 749 CCCCTGGCCGTGGGCATCG-CCTTCTTCCTCATGACGTTCT-TGGCCTCCTAGCTCT-GC Length 552; 1 others Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus troppicalis EST project 2001 TROPICALIS_SEQUENCE_ID: TGas008p08.sp6 Sequencing primer: SP6 979 AGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAG 1017 27.9%; Score 289.6; DB 9; 72.9%; Pred. No. 1.3e-37; /organism="Silurana tropicalis" 104 t б mRNA sequence. AL628407 AL628407.1 GI:16597890 western clawed frog. 186 c Query Match
Best Local Similarity 72.95
Matches 398; Conservative Sanger Centre οy

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/tissue_type="melanotic melanoma, high MDR"
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Best Local Similarity 90.4%;
Matches 320; Conservative
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                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                     Query Match
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DEFINITION
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AW200648
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummanlai Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammanlai Eutheria; Primates; Catarrhini; Hominidae; Homo.

Matchoal 10879)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/TD/DTP

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://mage.lnl.gov

Plate: LLCM173 row: e column: 15

High quality sequence stop: 494.
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                                                                                                                                                                                                                                  190 CTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAA 249
                                                              310 ACCGGGGCCCGGAGGCGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTA 369
                                                                                                                                                                                       GCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTA 489
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/db_xref="taxon:9606"
/clone="IMAGE:4305782"
/clone_lib="NIH_MGC_62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BF977204
BF977204.1 GI:12344419
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Xenopodinae; Xenopus.

Xenopodinae; Xenopus.

(I (bases 1 to 460)

Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person, Waterston,R. and Wilson,R., Ritter,E., Jackson,Y., McCann,R., Washu Xenopus EST project, 1999

Unpublished (1999)

Other_ESTs: daz4c06.1

Contact: Sandy Clifton, Ph.D.

Washu Xenopus EST project, 1999

Tel: 314 286 1800
/lab_host="DH108 (TI phage-resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggocgcccggcc); Site_2: sfil (ggocgctcggcc);
Double-stranded cDNA was prepared from cell line RNA. 5,
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATATGCCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCAATC-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 AAGACTTTGAGGGAGGAGACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCA 728
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Pred. No. 3.7e-34;
0; Mismatches 31
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6022737,
60227, MIH_MGC_84 Homo sapiens cDNA clone IMAGE:4360358 5',
mRNA section of
                                                                                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1013)
NHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10001 row: g column: 15
High quality sequence stop: 715.
Location/Qualifiers
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                                                                                                                                       BF969747.1 GI:12336962
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98.5%;
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                                                                                                  mRNA sequence.
BF969747
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AUTHORS
TITLE
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KEYWORDS
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BF969747
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                                                                                                                                                                                                                                          /clone="IRROPUGE_SOURCE_ID: Xinga003n11"
/clone="IRROPUGE_SOURCE_ID: Xinga003n11"
/clone=lib="normalized Xenopus laevis gastrula"
/tissue_type="gastrula" (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F""
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; DNA was prepared from 2ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae).
ECORI-Xhoi cut cDNA was then ligated into Unizap-XR (Stratagene) with EcoRI at the 5' end and Xhoi at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library by contruction by Bruce Blumberg (cho et al. 1991 Cell 67, 1111-1120). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
              Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by Washington University Genome Sequencing Center.
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seg primer: -40RP from Gibco
High quality sequence stop: 423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 TTAACAGTTGCAGTTTGTCTCTTATAATGACGCTCCTGGCTTCC 460
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                                                                                                                                                                                         1. .460
/organism="Xenopus laevis"
/db_xref="taxon:8355"
est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 74.0%;
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
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ORIGIN
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5 862 744 ACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCT 803 TGCACCATACATCTGTGTCCGCCCCTCTACCCCTTCCCCCCCACGTAGGGCACTGTAGTG 982 TGCACCATACATCTGTGTGCCG-CCCCTCTACCCCCTTCCCCCCACGAGGGCACTGTAGTG 239 Gaps 1 ACCIGCCCTGGCCGTGGCCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCT 60 804 GCCCCCTCCCCT-GGGGGGGGAGAGAGGGGGGGGGGGTTGGAAGGAGCAGCAGCCTTTG GCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCC 2, DB 10; Length 1013; Score 247.8; DB 10; Length Pred. No. 8.2e-31; 0; Mismatches 2; Indels

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Simpson, A.J.
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BF950361.1 GI:12367636
   288 bp mRNA linear EST 21-APR-1997 brain I Homo sapiens CDNA 5' end similar to similar
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                                                                                                                                                             1 (bases I to 200).
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                     Fax: 3018699423
Email: arkerlav@tigr.org
Emoil: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
/dev_stage="fetus, 24 wks"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 GAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAG 568
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA338749 288 bp mRNA EST43752 Fetal brain I Homo sapiens cDNA 5' to tyrosine kinase receptor, mRNA sequence. AA338749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
/db_xref="ArC (inhost):102467"
/db_xref="taxon:9660"
/clone_llb="Fetal brain I"
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Pred. No. 1.2e-30;
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0
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Contact: Kerlavage, AR
                                                                     AA338749.1 GI:1991007
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96.9%;
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                                                                                                                          Homo sapiens
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                                                                                                        human.
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Matches 251;
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ACCESSION
VERSION
                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                DEFINITION
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ORIGIN
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AUTHORS
TITLE
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MEDLINE
COMMENT
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1. .258
/organism="Homo sapiens"
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/clone_lib="Null97"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: pucl8; Site_l: Smal; /note="Organ: nervous_normal; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products of site_2: Ludwig Institute for Cancer Research)
profiles into the pucl 18 vector. Reverse transcription of tissue mRnA and cDNA amplification were performed under low stringency conditions."

1 others
                                                                                                                                                      1 (bases 1 to 258)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Slmpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
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Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NNI187-041100-465-c09&t3=2000-11-04&t4=1)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671
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101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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High quality sequence start: 12
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Location/Qualifiers
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Matches 233; Conservative
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12
                                                                                                                               September 27, 2002, 22:43:05 ; Search time 74.08 Seconds
(without alignments)
356.852 Million cell updates/sec
                                                                                                                                                                                                               US-09-904-954-2
1301
1 MARAPLILILLUVPVPLLPL......REHLPLAVGIAFFLMTFLAS 238
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            747574 segs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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A_Geneseq_032802:*

| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
		æ				
Result No.	Score	Query Match	Query e Match Length DB	DB	ID	Description
	1111111	1 1 1 1 1		i		
1	1301	100.0	238	16		Human hek-L protei
7	1266			16	AAR82605	Eph transmembrane
m	437			17	AAR94766	Mouse EPH receptor
4	437			19	AAW71006	Amino acid sequenc
2	437			20	AAY06822	Human LERK-6 polyp
9	426.5		335	22	ABG27837	Novel human diagno
7	421			17	AAR94767	Chicken EPH recept
80	421			19	AAW71007	Amino acid sequenc
σ	415.5			17	AAR97854	Human AL-1, a liga
10	415.5			17	AAW02586	Lerk-7 protein. H
11	415.5			17	AAW00035	HEK4 binding prote

LERK-6 protein. M LERK-6 protein. M Murine LERK-6 poly B61 protein sequen EBP. Homo saphens EBP transmembrane eck receptor bindi Human PR0202 prote Truncated eck rece Ligand for recepto Ligand for Ligand	tumorigenesis;
184 17 AAW02587 184 17 AAR91283 184 17 AAR91283 184 12 AAR26820 205 15 AAR23634 205 16 AAR82604 205 18 AAR82604 205 18 AAR82604 7 208 22 AAB50990 7 218 21 AAB54058 171 18 AAW18081 2 167 18 AAW18080 2 167 18 AAW18079 151 18 AAW18079 2 167 18 AAW18079 1 107 17 AAR94768 1 104 22 AAR94768 1 104 22 AAR94682 1 104 20 AAR94615 2 1 104 17 AAR94615 3 3 3 17 AAW9655 3 3 3 17 AAR94655 3 3 3 3 17 AAR94655 3 3 3 3 17 AAR94655 3 3 3 17 AAR94655 3 3 3 17 AAR94655	ALIGNMENTS Idard; Protein; 238 AA. (first entry) protein. surface; tyrosine kinase receptor; Location/Qualifiers 119 /note= "signal peptide" 20238 93US-0109745. 93US-0114426. 93US-0101132. 94US-0240124. NEX CORP. Cerretti DP;
12 403 31. 14 403 31. 15 390 30. 16 390 30. 17 390 30. 18 390 30. 20 386 29. 21 386 29. 22 386 29. 24 377.5 29. 25 377.5 29. 26 377.5 29. 27 377.5 29. 28 364.5 29. 29 364.5 29. 30 30. 31 22. 32 334 22. 33 34 22. 34 22. 36 4.5 28. 37 4.5 28. 38 4.5 28. 39 30. 30 30. 31 32 39. 32 30. 34 22. 36 4.5 28. 37 4.5 28. 38 4.5 28. 39 4.5 28. 30 30. 31 32 39. 32 30. 33 4.5 28. 34 22. 36 4.5 28. 37 4.5 28. 38 4.5 28. 39 4.5 28. 30 4.5 28. 31 4.5 28. 32 4.5 28. 33 4.5 28. 34 22. 36 4.5 28. 37 4.5 28. 38 4.5 28. 39 4.5 28. 30 4.5 28. 31 4.5 28. 32 4.5 28. 33 4.5 28. 34 5.5 28. 36 4.5 28. 37 4.5 28. 38 4.5 28. 39 4.5 28. 30 179 13. 30 179 13. 40 171.5 13. 41 171.5 13.	RESULT 1 AAR71481 XX AC AAR71481 standard; XX AC AAR71481; XX XX Human hek-L protein XX Ligand; cell surfa XX Ligand; cell surfa XX Homo sapiens. XX YX Homo sapiens. XX YX

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Efl-2 (also known as EHK-IL) is an Eph transmembrane tyrosine kinase family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2 ends in a C-terminal hydrophobic sequence that appears to to be a recognition sequence allowing it to be GPI-linked and thus lacking in an intracellular domain. Efl-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligands which bind Eph family receptors - used in the diagnosis
                                                                                                                                                                         Goldfarb M, Maisonpierre PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor ligand; dementia; tachycardia; therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.3%; Score 1266; DB 16;
98.3%; Pred. No. 2.8e-120;
ive 0; Mismatches 0;
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21..209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR94766 standard; Protein; 209 AA
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse EPH receptor ligand Elf-1.
                                                                                                                                                                         Gale N,
                                  94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
95WO-US04208
                                                                                                                                  (REGE-) REGENERON PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.3
Best Local Similarity 98.3
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                            neurological disorders
                                                                                                                                                                         Davis S,
                                                                                                                                                                                                                                 WPI; 1995-358635/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AA;
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                                  21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
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04-APR-1995;
                                                                                                                                                                                               Vancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1996
                                                                                                                                                                         Aldrich TH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 iycphynssgvgpgagpgpgggaegyvlymvsrngyrtcnasggfkrwecnrphaphspi 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorisenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytocoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                      New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 1301; DB 16; Length 238; Best Local Similarity 100.0%; Pred. No. 8.1e-124; Matches 238; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ef1-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
neurological disorder; identification; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "residue borders main conserved regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eph transmembrane tyrosine kinase family ligand, Efl-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPI-recognition tail"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR82605 standard; Protein; 234 AA
                                                                                                                                                   Claim 21; Page 36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-1996 (first entry)
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                WPI; 1995-106811/14
                                                                                                                                                                                                                                                                                                                                                                                                        238 AA;
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121

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181

AAR82605

Peptide Region

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Gaps

4,

Indels

Length 234;

of

20-OCT-1998 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15008) obtd. from an embryo mid- and hind-brain cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 agrpllpllll----llplrarnedparanadryavywnrsnprfqvsavgdgggytvev 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAPLILILILVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine and chicken EPH receptor ligand, {\rm Elf}-1 - useful in diagnosis and treatment of disorders associated with the {\rm Elf}-1 gene, e.g. dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                /note= "potential N-glycosylation site"
170
                                                                                                                                                        /note= "potential N-glycosylation site"
                                                                                                                 /note= "potential N-glycosylation
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.6%; Score 437; DB 17;
50.5%; Pred. No. 3.6e-36;
iive 25; Mismatches 47;
           69.159
/label- Cys4_motif
35.166
/label- Core_sequence_motif
 /label- Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                              95US-0393462.
                                                                                                                                                                                                                                                95WO-US11869
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Best Local Similarity 50.5
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                             Cheng H, Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-188446/19.
N-PSDB; AAT15008.
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                                                                         Modified-site
                                                                                                        Modified-site
                                                                                                                                      Modified-site
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19-SEP-1994;
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AAW71006 standard; Protein; 209 AA.

AAW71006;

AAW71006
ID AAW7
XX
AC AAW7
XX

RESULT

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7;
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                                                         Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracelulular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 22;
                                                                                                                                                                                                                                                                             'note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                          /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 209;
                                                                                                                                                                                                                                                                                35.1166 Forestrian N-11nked glycosylat 35.1166 /note= "contains core sequence motif" 69.159
                           Amino acid sequence of a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 437; DB 19;
; Pred. No. 3.6e-36;
25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                           /note= "contains a Cys4 motif"
                                                                                                                                                                                                             /note= "signal peptide"
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2A; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.6%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0455001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheng H, Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-466665/40.
N-PSDB; AAV42926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥,
                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                         bone formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
                                                                                                                                                                                                                                                                                                                                                            Mod1fied-site
                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                         US5795734-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                  Protein
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us-09-904-954-2.rag

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The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the cohancement, stimulation, proliferation or growth of cells expressing the chart of all receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural itssue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating cure undergenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the energy or the elk or hek cell surface receptor. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                            LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease; neurodegenerative; excitotoxicity.
                                                                                                                                53
                                  59
AAAPLLELLLUVPVPLLPLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV
                  NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                              AAY06822 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 42; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US17772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0920440
                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Human LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-243567/20.
N-PSDB; AAX32767.
                                                                                                                                                                                                SHSGEKPVPT 180
                                                                                                                                                                                                                               173 lyeapepift 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                AAY06822;
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                                                                                                                                                                                                                            PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                   Gaps
                                                                                       2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV
                                                                                                                                        NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                   18;
 Length 213;
                                   Indels
33.6%; Score 437; DB 20;
llarity 50.5%; Pred. No. 3.7e-36;
Conservative 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 58196; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #27828.
                                                                                                                                                                                                                                                                                                                                                                                               ABG27837 standard; Protein; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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N-PSDB; AAS92024.
                                                                                                                                                                                                                                                                            171 SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                            177 lyeapepift 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                 1 Similarity
96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG27837;
   Query Match
Best Local 8
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                                                                                                                                        54
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                                   Matches
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31-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                           AAW71007;
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                173
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AAW71007
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                                                                                                              . 11;
responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                             106 lgvapvemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyl 165
                                                                                                                                                                DIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHS 118
                                                                                                              Gaps
                                                                                                                                                                          MAAAPLLLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYL
                                                                                                                                                                                                119 PIKFSEKFORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHS
                                                                                                                                                                                                          174 GEKPVPTLPQFTMGPNVKINVLEDFE------GEN-PQVPKLEKSISGTSPKREH
                                                                                                                                                                                                                                              47;
                                                                                             Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                   dementia; tachycardia; therapy;
                                                                                            ; Score 426.5; DB 22; Length
; Pred. No. 7.8e-35;
39; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Sig_peptide
22..200
/label- Mat_protein
61..150
/label- Cys4_motif
33..157
/label- Core_sequence_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              AAR94767 standard; Protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                  receptor ligand Elf-1.
                                                                                                                                                                                                                                                                                                                                                                                                 receptor ligand; d
transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                           Query Match
Best Local Similarity 39.29
Matches 100; Conservative
                                                                                                                                                                                                                                                                   222 LPLAVGIAFFLMTFL 236
                                                                                                                                                                                                                                                                                 ---llaillflaml 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng H, Flanagan JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                  Chicken EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                   EPH
                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
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                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; E61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elf-1 (AAR94767), is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 cphyee-----plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk 112
                                                                                                                                                                                                                                                                                                                    the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AATISO09) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AAPLLLLLLVPVPLLPLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 aaallaaivgvcv----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy 60
                                                                           Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g. dementia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "contains a core sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 421; DB 17;
Pred. No. 1.4e-34;
9; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of an avian Elf-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "contains a Cys4 motif"
                                                                                                                                                                                                                                                                                       novel chicken EPH receptor ligand,
                                                                                                                                                                                                                        Claim 1; Page 88-89; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
61..150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW71007 standard; Protein; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%; Scoilarity 47.5%; Proc
Conservative 29;
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35..157
/note= "c
WPI; 1996-188446/19.
N-PSDB; AAT15009.
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Best Local Similarity
Matches 86; Conserv
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Misc-difference
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/label- Sig_peptide
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Matches 98; Conservative
                                                                                                                                214..228
                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                Caras IW, Winslow JW;
                                                                                                                                                                                                                                                                                                                      WPI; 1996-239448/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AA;
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                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT18897
             Modified-site
                                              Modified-site
                                                                                  Binding-site
                                                                                                                                                                   WO9613518-A1
                                                                                                                                                                                                                                                27-0CT-1994;
                                                                                                                                                                                                                26-OCT-1995;
                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                        09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                  Domain
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                                                                                                                                                                                                The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a phyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended fo transphatation), also therapeutically in increase neuron survival e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 CPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 cphyee-----plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAPLILLILUVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                              Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL-1; REK7; eph-related tyrosine kinase receptor; ligand;
neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                               32.4%; Score 421; DB 19;
47.5%; Pred. No. 1.4e-34;
ative 29; Mismatches 50;
                                                                                                                                                                             Claim 1; Columns 75-78; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR97854 standard; Protein; 228 AA.
95US-0455001.
94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                              (HARD ) HARVARD COLLEGE.
                                                                      Cheng H, Flanagan JG;
                                                                                           WPI; 1998-466665/40.
N-PSDB; AAV42927.
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             200 AA;
 31-MAY-1995;
19-SEP-1994;
                       27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 T 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR97854;
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related tyrosine kinase receptor REK7 (AAR97853). Its amino acid sequence was deduced from a cDNA clone (AAT18897) isolated from a human foetal brain cDNA library. Recombinant, mature AL-1 can be produced in transformed host cells. It may be useful in promoting the development, maintenance or regeneration of neurons in vivo, and can be utilised in methods for the diagnosis and/or treatment of neurological disorders. It can also be used to promote or enhance angiogenesis. Antegonists and agonists of AL-1, as well as antibodies raised against AL-1, also have therapeutic applns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :: ||||:|| | ||:|||:
118 fqlftpf8lgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 NSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \Delta L-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.9%; Score 415.5; DB 17; Length 39.5%; Pred. No. 6.1e-34; ive 37; Mismatches 66; Indels
37..39
/label= Glycosylation
/note= "potential N-glycosylation site"
162..164
/label= Glycosylation
/note= "potential N-glycosylation site"
203..204
                                                                                                                                                                                                                                             glycophosphatidyl-inositol"
                                                                                                                                                                                                                      /label= GPI
/note= "potential attachment site
                                                                                                                                                                                                                                                                                                                                                  /label- Hydrophobic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anglogenesis-related conditions.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW00035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human Lerk-7 cytokine - which binds to cell surface receptors elk, hek and eck, useful for delivering agents to cells or for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
Lerk-7; probe; cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                              ...133
|Tabel= extracellular_receptor-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
/label= GPI_attachment_site
                                                                                                                                                                                                                                                                                                                                                                           1..228
/label= precursor_protein
                                                                                                                                                                                                                                                                                                                                                       'label- signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spacer_region
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 37-38; 49pp; English.
                                  AAW02586 standard; Protein; 228 AA.
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                                                                                                                 (first entry)
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/label= s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                      Lerk-7 protein.
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1995;
06-DEC-1994;
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                                                                                                                 28-NOV-1996
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                                                                          AAW02586;
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                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                   Oomain
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10
RESULT
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11;

Gaps

47;

Ouery Match
Best Local Similarity 39.5%; Pred. No. 6.1e-34;
Matches 98; Conservative 37; Mismatches 66; Indels 47;

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Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates HEK4 and ECK receptors. Its amino acid sequence was deduced from a cDNA clone (AAM134292) isolated from a human placenta cDNA library. Expression vectors and host cells can be used for the prodn. of biologically active HEK BP. It is useful for modulating the growth and/or differentiation of EGH sub-family receptor-bearing cells, esp. in liver, kidney, lung, skin or neural tissues. It can be used to treat neural system disorders and in the regeneration of
                                                                                                                                                                                             6 eds-----vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek 117
                                                                                                                                                                                                                                                                                                           126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                       || :: ||||:|| | ||:|||: | ||::|||| | ::
fglftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to modulate growth and differentiation of, e.g. liver and kidney cells, and to treat cancer and nervous system disorders
                                                                    65
                                    HEK4 binding protein; HEK4 receptor; EPH-like receptor; protein tyrosine kinase; ligand; growth; differentiation; cancer; nervous system disorder; therapy; antibody.
                                                                                                                                                 67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK
LLLLLVPVPLLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
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20..228
/label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEK4 binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-362633/36.
N-PSDB; AAT34292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 AFFLMTFL 236
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218 11fllaml 225
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5

Gaps

16;

40; Indels

Length 184;

DB 17;

Score 403; DB 17; Pred. No. 8.5e-33;

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and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                            82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                                                                                                                                          | :|:||||| || : ||||| || 3 anadryavywnrsnprfqvsavgdgggytvevsindyldiycphy-----gaplppae 55
                                                                                                                                                 28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGFG 81
                                                                                                                                                                                                                                       141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                            31.0%; Scotts 50.6%; Pred. No. cotts 50.6%; Mismatches
                                                                                                                            Conservative
                                                                                                     Query Match
Best Local Similarity
                                                                    184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT14009
                                                                                                                                                                                                                                                                                                                                                                                       LERK-6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9610911-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                10-0CT-1996
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                                                                                                                            82;
                                                                                                                                                                                                                                                                                                                                         AAR91283;
                                                                      Sequence
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                                                                                                                             Matches
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                                                                                                                                                                                                     FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                   67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                        181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                             Gaps
                                                                                                              8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                            to cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                hek; elk; cell surface receptor; culture; reagent;
disorder; injury; delivery agent; diagnostic; therapeutic;
probe; cytokine.

    which binds to cell surface
for delivering agents to cells

  tissues. Antagonists are useful for cancer can also be used to raise antibodies.
                                                                                          47;
                                                                    Length 228;
                                                                                          Indels
                                                                    DB 17;
                                                                                          99
                                                                    Score 415.5; DB 1
Pred. No. 6.1e-34;
                                                                                         37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human Lerk-7 cytokine receptors elk, hek and eck, useful for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                         AAW02587 standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 35; 49pp; English.
                                                                    31.9%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0396946,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US15781
                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-1996 (first entry)
                                                                                         98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
   damaged or depleted
               HEK4 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-287171/29.
N-PSDB; AAT32700.
                                                                             Local Similarity
                                   228 AA;
                                                                                                                                                                                                                                                                                            229 AFFLMTFL 236
                                                                                                                                                                                                                                                                                                                 218 11filaml 225
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lerk-6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-1996
               treatment.
                                                                                                                                                                                                                                                                                                                                                                                               AAW02587;
                                    Sequence
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lerk-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lerk-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuron;
                                                                                          Matches
                                                                                                                                                                                                     126
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The LERK-6 polypeptide encoded can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to hek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LERK-6; hek; elk; cell surface receptors; culture; reagent; neurons; disorder; injury; delivery agent; diagnostic; therapeutlc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated DNA encoding cytokine designated LERK-6 which binds tand elk cell surface receptors – useful for drug delivery and
AAR91283 standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 34; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contact with the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US12779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0538709
94US-0318393
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening procedures
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The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the enhancement, stimulation, proliferation or growth of cells expressing the neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating curvey degenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the large.
                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    injury;
disease;
                                                                                                                                                        82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                        28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG
                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity.
     Length 184;
                                       40; Indels
                                                                                                                                                                                                    141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                                                                                         Score 403; DB 17;
Pred. No. 8.5e-33;
24; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 37-38; 46pp; English.
                                                                                                                                                                                                                                                                                                                  AAY06820 standard; Protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cytokine designated LERK-6
      31.0%;
50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nurine LERK-6 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                  Murine LERK-6 polypeptide
                                       82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-243567/20.
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                  AAY06820;
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                                       Matches
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The B1 protein sequence was deduced from the cDNA sequence obtd. by screening a cDNA library from human umbilical vein endothelial cells with radiolabelled cDNA fragments derived from the 5' end of B61 DNA. The B1 protein has 205 residues (24 kD) comprising a signal sequence and hydrophobic N- and C- terminal regions. The B61 gene is involved in early inflammatory response and serves as a marker. It may be detected by probes or by antibody-based immunoassay of biological fluids such as plasma, CSF or urine. These assays make it possible to predict a worsening in a disease process and allow the quantitative assessment of the magnitude of the inflammatory response. This information will allow the earlier admin. of appropriate therapy, thereby shortening the disease process and limiting the patient's exposure to anti-inflammatory/immunocustive therapy. B61 induction is rapid and profound, hence
                                                                                                                              82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
                                                                                                                                                 28 ALGNRHAVYWNSSNQHLRRE-----GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                       Barly inflammatory response; marker; antibody; therapy; induction;
lipopolysaccharides; cytokines; Interleukin-2; IL-2; INF.
                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene prod. used as marker to detect inflammatory response - by detecting the B61 gene in biological fluids or by using hybridisation probes
 Length 184;
                                 Indels
                                                                                                                                                                                              141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                                                                                 ||||||||| || : : |||:||:| : |: :|: || 116 gheyyyisatppnlvdrpclrlkvyvrptnetlyeapepift 157
Score 403; DB 20;
Pred. No. 8.5e-33;
1; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                              24;
                                                                                                                                                                                                                                                                                                          AAR23895 standard; Protein; 205
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 31.0%;
50.6%;
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         861 protein sequence
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 Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ24595
                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-0CT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1992
                                                                                                                                                                                                                                                                                                                                         AAR23895;
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Peptide
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                                                                                                                                                                                                                                                                                                           138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                          Ouery Match 30.0%; Score 390; DB 13; Length 205; Best Local Similarity 41.8%; Pred. No. 2.1e-31; Matches 87; Conservative 21; Mismatches 76; Indels 24; Gaps
                                                                                                                                                                                                               19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                                    it is easily detectable. The B61 response is highly specific to proinfilammatory stimuli, being only made by cells exposed to lipopolysaccharides or cytokines such as IL-2 and TNF and not growth factors or interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                   198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| | :| | :| | :|:
----pevrvlhsighsaaprl--fpla 191
                                                                                        205 AA;
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Search completed: September 28, 2002, 01:36:51 Job time: 10426 sec

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Database

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COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version: 5.1a
SOFTWARE: Microsoft Word for Apple, Version: 5.1a
SOFTWARE: Microsoft Word for Apple, Version: 5.1a
SOFTWARE: Willow DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHEYN A.
REGISTRATION NUMBER: 32.172
REGISTRATION NUMBER: 32.172
REGISTRATION NUMBER: 32.172
REGISTRATION NUMBER: 32.172
              US-08-321-162-2
US-08-448-736-1
US-08-448-736-1
US-08-452-779-1
US-08-45-065-1
US-08-45-065-1
US-08-959-524-1
US-08-959-524-12
US-08-959-524-12
US-08-959-524-12
US-08-959-524-12
US-08-959-514-12
US-08-959-514-12
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US-08-453-943-4
US-09-057-121-4
US-09-358-734-4
US-09-609-324A-8
US-08-920-440B-8
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08240124
Sequence 2, Application US/08240124
Fatent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECRMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT B TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCES: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATILE
CTATE: SEATILE
COUNTRY OF SECULATION
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TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206) 587-0430
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-240-124-2
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3Y: linear
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September 27, 2002, 22:50:00 ; Search time 29.18 Seconds
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                                                                                                                                                                                                                  US-09-904-954-2
1301
1 MAAAPLLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238
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Sequence 4
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/be_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-920-440B-10
US-09-173-492-10
US-09-173-133-10
US-08-455-001-4
PCT-US95-11869-4
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US-08-299-567-5
US-08-455-001-2
US-08-308-814-2
PCT-US95-11869-2
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US-08-440-815-4
US-08-379-802-2
US-09-048-129-2
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US-08-486-449-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
Sequence:
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; MOLECULE TYPE:
US-08-453-943-2
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US-09-057-121-2
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TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: 1MANUREX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: MASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Machinosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 30-MAY-1995
CLASSIFICATION NUMBER: US 08/161,132
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-MG-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-MG-1933
PRIOR APPLICATION NUMBER: 30-MG-1933
ATTORNEY APPLICATION DATA:
APPLICATION NUMBER: 05 08/109,745
FILING DATE: 30-MG-1933
ATTORNEY APPLICATION NUMBER: 105 08/109,745
FILING DATE: 20-MG-1933
ATTORNEY APPLICATION NUMBER: 20-MG-1933
ATTORNEY APPLICATION NUMBER: 20-MG-1993
                                             Query Match 100.0%; Score 1301; DB 1; Length 238; Best Local Similarity 100.0%; Pred. No. 2.7e-128; Matches 238; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REGERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-453-943-2; Sequence 2, Application US/08453943; Patent No. 5738844; GENERAL INFORMATION:
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INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 238 amino acids TYPE: amino acid
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; Sequence 2, Application US/09057121
; Patent No. 5969110
; GENERAL INFORMATION:
    APPLICANT: BECKMANN, M. P.
    APPLICANT: BECKMANN, M. P.
    TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
    TITLE OF INVENTION: RECEPTOR HEK
    NUMBER OF SEQUENCES:
    ADDRESSEE: IMMUNEX CORPORATION
    STREET: SI UNIVERSITY STREET
    CITY: SEATLE
    STATE: WASHINGTON
    COUNTRY: USA
                                                                                   Length 238;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: Apple System 7.1 Microsoft Word for Apple, Version 5.1a
                                                                               ; Score 1301; DB 1;
; Pred. No. 2.7e-128;
0; Mismatches 0;
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APPLICATION NUMBER:
FILING DATE:
03-DEC-1993
FILING DATE:
03-DEC-1993
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
30-AUG-1993
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
ELLING DATE:
CLASSIFICATION:
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APPLICATION NUMBER: 08/240,124
                                                                                   100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacLintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 amino acids
                                                                                 Query Match
Best Local Similarity 100.0
Matches 238; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
protein
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61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
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                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. 5747033
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
                                                                                                            Score 1301; DB 4;
Pred. No. 2.7e-128;
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Pred. No. 4e-124;
); Mismatches
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777 Old Saw Mill River Road
                                                                                                                                                0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,143
                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 238; Conservative 0;
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Best Local Similarity 97.9
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-299-567-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron
                                ; MOLECULE TYPE: protein US-09-358-734-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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  amino acid
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                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURREMY APPLICATION DATA:
                                                                                                            Query Match 100.0%; Score 1301; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-128; Matches 238; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUUKESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET CITY: SEATTLE STATE: WASHINGTON COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/358,734 FILING DATE: CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09358734 Patent No. 6274117 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 233-0644
TELEEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 amino acids
              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-057-121-2
amino acid
                                                                                                            Query Match
Best Local Similarity
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Sun Sep 29 08:45:20 2002

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171 SHSGEKPVPT 180

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                                                                                 54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
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22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.6%; Score 437; DB 1; Length 209; 50.5%; Pred. No. 5.4e+38; Live 25; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPKX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CARRACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: ASCII (Lext)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILLING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATYORNEY APPLICATION: 800
                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08455001
Patent No. 5795734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.59
Matches 96; Conservative
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US-08-455-001-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: PH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHLYE & COCKFIELD
STREET: 60 State Street
CITY: BOSCON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Indels
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50.5%; Pred. No. 5.4e-38;
iive 25; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(KAX)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,814
FTILING DATE: 19-SEP-1994
CLASSIFICATION NUMBER: 036.709
REGISTRATION NUMBER: 36.709
REGISTRATION NUMBER: HMI-011
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-75941
INFORMATION FOR SED ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application PC/TUS9511869
                                                                                                               Sequence 2, Application US/08308814
Patent No. 6268476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 209 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.6
Best Local Similarity 50.5
Matches 96, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-308-814-2
173 LYEAPEPIFT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 SHSGEKPVPT 180
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PCT-US95-11869-2
                                                                                       US-08-308-814-2
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113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
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                                                                                                                                                                                                           54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                    2 AAAPLL-LILLIVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53
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                                       Length 213;
                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPPRATIG SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/920,440B
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08920440B
Patent No. 591905
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION:
UNBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                       ; Score 437; DB 1;
; Pred. No. 5.6e-38;
24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.6%; Score 437; DB 2; Best Local Similarity 50.5%; Pred. No. 5.6e-38; Matches 96; Conservative 24; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                     33.6%;
ilarity 50.5%;
Conservative 2
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                                          Query Match
Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAAPLLLLLLLLVPVPLLPLLA - OGPGGALGNRHAVYWNSSNQHLRRE - - - - - GYTVQV 53
                                          EPH Receptor Ligands, and Uses Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
FILE REFERENCE: A772
CURRENT APPLICATION NUMBER: US/09/609,324A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 08/920,440
PRIOR APPLICATION NUMBER: 08/538,709
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-39
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VET: 2.1
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%; Score 437; DB 5;
illarity 50.5%; Pred. No. 5.4e-38;
Conservative 25; Mismatches 47
                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRA: (617) 227-7400
TELERAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
GENERAL
APPLICANT:
TITLE OF INVENTION: EPH RECELL
TITLE OF SEQUENCES: 5
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CVSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-609-324A-10
; Sequence 10, Application US/09609324A
; Patent No. RE37582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT-US95-11869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 96; Conserv
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; ORGANISM: LERK-6
US-09-609-324A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-09-173-133-10
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64 SINDYLDIYCPHY-----GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116
                                113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                    54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAAPLL-LLLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-----EGYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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                                                                                                                                                                                                                                                                                                                                                         STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,492
                                                                                                                                                                                                                       Sequence 10, Application US/09173492
Patent No. 6194172
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 213 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-173-492-10
                                                                                                                         : :|: |
177 LYEAPEPIFT 186
                                                                                                   171 SHSGEKPVPT 180
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Best Local Similarity
Matches 96; Conserva
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                                                                                                                                                                                                        US-09-173-492-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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64 SINDYLDIYCPHY-----GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 NVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 213;
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Sequence 10, Application US/09173133
Patent No. 6232447
GENERAL INFORMATION:
CENTEAL INFORMATION:
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                 ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%; Score 437; DB 4;
50.5%; Pred. No. 5.6e-38;
iive 24; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICOR APPLICATION
PRICOR APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826-B
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 233-0430
TELEFAN: (206) 233-0430
TELEFAN: (206) 233-0444
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
(US-08-455-001-4
) Sequence 4, Application US/08455001
) Patent No 579534
) GENERAL INFORMATION:
APPLICANT: Planagan, John G.
APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 213 amino acids
amino acid
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Best Local Similarity 50.5%
Warches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-173-133-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                               98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CPHYEE-----PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                  3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AAALLAAIVGVCV-----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60
                                                                                                                                                                                                                                                                                                                               Length 200;
                                                                                                                                                                                                                                                                                                                             Query Match 32.4%; Score 421; DB 5; Best Local Similarity 47.5%; Pred. No. 2.4e-36; Matches 86; Conservative 29; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08442248
Patent No. 5759863
GENERAL INFORMATION:
APPLICANT: Winslow, John W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .олы ЕК: US/08/442,248
15-MAY-1995
N: ^^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                        TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              : 200 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torchia, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415/952-9881
                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein PCT-US95-11869-4
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US-08-442-248-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
WUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related TITLE OF INVENTION: Thereto Thereto SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%; Score 421; DB 1; Length 200; ilarity 47.5%; Pred. No. 2.4e-36; Conservative 29; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII (Text)
CURRENT APPLICATION DATA:
PELLING DATE: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY, FAGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
PCT-US95-11869-4
; Sequence 4, Application PC/TUS9511869
; GENERAL INFORMATION:
                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 200 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 86; Conserva
                                                                                                                                                                02109
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181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
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                                                                                                                                                                                                                                                          Query Match 31.9%; Score 415.5; DB 1; Length 228; Best Local Similarity 39.5%; Pred. No. 1.1e-35; Matches 98; Conservative 37; Mismatches 66; Indels 47;
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-442-248-4
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218 LLFLLAML 225
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Search completed: September 28, 2002, 01:37:42 Job time: 10062 sec

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(without alignments)
333.312 Million cell updates/sec
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1301
1 MARAPLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       3502263 seqs, 351980561 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pending_Patents_AA_Main:*
                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                    Run on:
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:* 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:* 25: /cgn2_6/ptodata/2/paa/US100_COMB.pep:* 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptcdata/2/paa/US092_COMB_pep:*
/cgn2_6/ptcdata/2/paa/US093_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US094_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US095_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US095_COMB.pep:*
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/cgn2__6/ptodata/2/paa/US088_COMB.pep:* /cgn2__6/ptodata/2/paa/US089_COMB.pep:* /cgn2__6/ptodata/2/paa/US090_COMB.pep:*

/cgn2_6/ptodata/2/paa/US090_COMB. /cgn2_6/ptodata/2/paa/US091_COMB.

SUMMARIES

		Description		Sequence 2, Appli	Sequence 315, App	360,				
		ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PCT-US94-09282-Z	US-08-109-745-2	US-08-161-132-2	US-09-733-756-2	US-09-904-954-2	US-09-948-941-315	US-09-948-941-360
		DB	Ι,	-	Ŋ	Ŋ	21	23	23	23
		Length		238	238	238	238	238	238	238
æ	Query	Match Length DB ID		100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	, ,	130T	1301	1301	1301	1301	1301	1301
	Result	No.		⊣	7	m	4	S	9	7

	Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 2, Appli
0 US-08-730- 0 US-08-327-4 US-08-327-4 US-08-327-4 US-08-231-6 US-09-621- 6 US-60-207- US-08-222-0 US-08-222-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-223-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-221-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0 US-08-231-0	5 US-09-135-12 US-08-330-128 US-08-440-567 US-08-442-245 US-08-542-245 US-08-542-245 US-08-542-245 US-08-542-245 US-08-542-63 US-08-570-32-66 US-08-318-36-946 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-38-709 US-08-318-768 US-08-318-768 US-08-318-768
7 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	200 2228 2228 2228 2228 2228 2228 11884 11884 11884 1484 1884 18
88799949744EEEEUUUUUU	33112 33113 33113 3313 3313 3313 3313 3
1285.5 1285.5 1285.5 1286.5 1126.5 1250.5 1250.5 1250.5 444.4 444.5 444.5 444.5 437 437 437 437 437 437 437 437 437 437	4 4 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
8 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2000 2000 3000 3000 3000 3000 3000 3000

ALIGNMENTS

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RESULT

PCT-US94-09282-2;
Sequence 2, Application PC/TUS9409282

Sequence 2, Application PC/TUS9409282

GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATLE: WASHINGTON
COUNTR: MASHINGTON
COUNTR: MASHINGTON
COUNTR: PADDLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: MICROSOFT WORD ATA:
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: MICROSOFT WORD ATA:
CHASIFICATION NUMBER: PCT/US94/09282
FILING DATE:
CLASSIFICATION NUMBER: US 08/161,132
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
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FILING DATE:
                                                                                                                           TOPOLOGY:
            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAAPLILLLLIVPVPLEPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1301; DB 1; Length 238; ilarity 100.0%; Pred. No. 2.5e-123; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: SI UNIVERSITY STREET
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: STADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macinicosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word, Version 5.1
SOFTWARE: Microsoft Word, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,745
FILING DATE: 20-Aug-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814
TELECHONE: (206) 587-0430
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHEYN A.
REGISTRATION NUMBER: 2814-C
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 233-0644
TELEFAX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local Simi
Matches 238;
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                                                                                                                                                                                                                                                                                                                                                                                                    1 MAAAPLILILILVPVPLLPFLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                             Length 238;
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US-08-161-132-2
Sequence 2, Application US/08161132
Sequence 2, Application US/08161132
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,132
                                                                                                                                                                                                                                                                     100.0%; Score 1301; DB 5;
100.0%; Pred. No. 2.5e-123;
ive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A:
REGISTRATION NUMBER: 32,172,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
          TELEX: 756822
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 238 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
(206) 233-0644
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Best Local Similarity 100.0
Matches 238; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-109-745-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
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61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
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                                              181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS
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100.0%; Pred. No. 2.5e-123;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA: US/09/904,954
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: <UNknown>
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FILING DATE: <URNOWN>
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                       CERRETII, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear;
HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-904-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
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TELEFAX: (206) 233-0644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            Sequence 2, Application US/09904954 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 238; Conservative
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GENERAL INFORMATION:
APPLICANT: Wack, Dawled
APPLICANT: Walson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER AND/OR BREAST CANCE
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER AND
TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER AND
FRIOR APPLICATION NUMBER: US 09/493,444
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-112-02
PRIOR FILING DATE: 1999-112-02
PRIOR APPLICATION NUMBER: PCT/US 00/07044
PRIOR APPLICATION NUMBER: PCT/US 00/07044
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PALENTIN VEFSION 3.1
SEQ ID NO 2.3
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                                                                                                                                                                                                                                                                                                                                                                                                                     61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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                                                                                                                                                                                                                                                                       1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 238;
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100.0%; Pred. No. 2.5e-123;
iive 0; Mismatches 0;
                                                                                                                                                             100.0%; Score 1301; DB 5;
1larity 100.0%; Pred. No. 2.5e-123;
Conservative 0; Mismatches 0:
238 amino acids
amino acid
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Best Local Similarity 100.
Matches 238; Conservative
                                                                     ; MOLECULE TYPE: protein US-08-161-132-2
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; ORGANISM: Homo sapiens
US-09-733-756-2
                                                   linear
                                                                                                                                                                                            Local Similarity
nes 238; Conserv
                       TYPE: ami
TOPOLOGY:
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Best Local S.
Matches 238
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121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                   181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPRREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                         DB 11; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
TITLE OF INVENTION: Method of Activating a Novel Ligand
TITLE OF INVENTION: Regulatory Pathway
TUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Room 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1285.5; DB 11; Lengt
Pred. No. 9.3e-122;
0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,700A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,518
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-730-700A-16
; Sequence 16, Application US/08730700A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-586-3135
TELEFAX: 416-586-3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.88;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.6
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronco
STATE: Ontario
COUNTRY: Canada
7IP: M5G 1X5
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STREET: buc.
TTOORTO
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                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: PUTTH CANCER, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOO788
CURRENT APPLICATION NUMBER: US/09/948,941
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 12618
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 360, Application US/09948941
GREEAL INFORMATION:
GREEAL INFORMATION:
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000788
CURRENT APPLICATION NUMBER: US/09/948,941
CURRENT FILING DATE: 2001-09-10
PRIOR RELING DATE:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 1301; DB 23; Length 238; Best Local Similarity 100.0%; Pred. No. 2.5e-123; Matches 238; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1301; DB 23;
100.0%; Pred. No. 2.5e-123;
tive 0; Mismatches 0; 1
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 360
LENGTH: 238
                                                                                                                            Sequence 315, Application US/09948941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-09-948-941-315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-09-948-941-360
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US-08-229-402-7
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Best Local S
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                                               LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                      Henkemeyer, Mark
TITLE OF INVENTION: Method of Activating a Novel Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/621,595
FILING DATE: 21-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 9.3e-122;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.8%; Score 1285.5; 99.6%; Pred. No. 9.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: KUTOYOYK, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/POCKET NUMBER: 3153-196
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      Regulatory Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:.protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-621-595-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/730,700
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Room 970
STREET: 600 University Avenue
CITY: Toronto
                                                                                                                                                                  Sequence 16, Application US/09621595
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 416-586-3235
TELEFAX: 416-586-3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1X5
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.8 Best Local Similarity 99.6 Matches 237; Conservative
                                                                                                                                 RESULT 9
US-09-621-595-16
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121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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Pred. No. 8.8e-120;
                                                                                                             ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Sequence 7, Application US/08229402
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TILLE OF INVENTION: EPH Family Ligands
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/144,992
FILING DATE: 15-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/736,559
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,402
FILING DATE: 12-APR-1994
CLASSIFTCATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,075
FILING DATE: 04-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 914-347-2113
INFORMATION FOR SEQ ID NO: 7:
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Similarity 98.3%;
                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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RESULT

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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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Pred. No. 2.8e-119;
0; Mismatches 1; Indels
               Sequence 5, Application US/08327423

GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COWTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TYPE: Floppy disk
COMPUTER TYPE: Floppy disk
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GENERAL INFORMATION:
APPLICANT: Peavson, Anthony
APPLICANT: Henkemeyer, Mark
TITLE OF INVENTION: Method of Activating a Novel Ligand
TITLE OF INVENTION: Regulatory Pathway
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 21-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,567
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kempler, Gall M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.9%;
Matches 233; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-327-423-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
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US-08-327-423-5
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1 MAAAPLILILILVPVPLLPLIAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.1%; Score 1250.5; DB 11; Length 233; 97.9%; Pred. No. 3.3e-118; 1.1ve 0; Mismatches 0; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-OW-02-1737-17
Sequence 15, Application US/09621595
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: Method of Activating a Novel Ligand
Regulatory Pathway
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,700A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Room 970
STREET: 600 University Avenue
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,518
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        PC-DOS/MS-DOS
                                    CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1X5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PatentIn Release #1.
ADDRESSEE: Room 970
STREET: 600 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REPERENCE/POCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-586-3235
TELEFAX: 416-586-3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 233 amino acids TYPE: amino acid STRANDEDNESS: single .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1X5
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-730-700A-15
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US-09-621-595-15
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Sequence 7, Application US/09214631
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: UNMBER: US/09/214,631
CURRENT PRILIG DATE: 1199-03-12
EARLIER APPLICATION NUMBER: CGT/CA97/00473
EARLIER FILING DATE: 1999-07-04
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 233
TYPE: PRT
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COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
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Pred. No. 3.3e-118;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORREY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-196
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/621,595
FILING DATE: 21-Jul-2000
CLASSIFICATION: <unh color of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-621-595-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/730,700 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 416-586-3235
TELEFAX: 416-586-3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 233 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 97.9%;
Matches 233; Conservative
READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Sequence 335. Application US/60212656
; Sequence 335. Application US/60212656
; Sequence 335. Application:
    APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
    TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000673
; CURRENT APPLICATION NUMBER: US/60/212,656
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                61 IYCPHYNSS----GAGPGPGGGAE-YVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 YEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL 195
                                                                                                                              1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                            18;
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                                                              Score 1227.5; DB 1
Pred. No. 7.2e-116;
0; Mismatches 4;
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; Pred. No. 1.6e-65;
17; Mismatches 43;
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Job time: 891 sec
                                                                94.4%;
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65.0%;
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                                                              Query Match
Best.Local Similarity 96.2
Matches 229; Conservative
; . ORGANISM: Homo sapiens US-09-214-631-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HUMAN
US-60-212-656-335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 335
LENGTH: 776
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510.684 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
Sequence:
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Maximum DB seq
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

(gnn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*
(gnn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*)
(gnn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*)
(gnn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*)
(gnn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*)
(gnn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*)
(gnn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*) Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Sequence Sequence Sequence Sequence sedinence sedine Sequence SUMMARIES DB Query Match Length Score Result . 0

sequence 288, App Sequence 288, App	Sequence 288, App
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US-10-121-045-288 US-10-121-046-288 US-10-121-051-288 US-10-121-048-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-121-052-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-124-812-288 US-10-123-288 US-10-123-288	US-10-123-236-3
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ALIGNMENTS

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APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Anonahan, John
APPLICANT: Monahan, John
APPLICANT: Manatkar, Shubhangi
APPLICANT: Galatt, Karen
APPLICANT: Gannavarapu, manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DEBTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CENVICAL CANCER
TITLE OF INVENTION: OF CENVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PELILNG DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-10-11-14
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                                                                                                                                                                                                                                                                                                                                              66 EDS------VPEDKTERYVLYMVNFDGYSACD4TSKGFKRWECNRPHSPNGPLKFSEK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LPQFTMGPNVKINVLEDFE------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
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                                                                                                                                                     47;
                                                                                                       Length 228;
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                                                                                                  Query Match 31.8%; Score 413.5; DB 6; Length 2 Best Local Similarity 39.5%; Pred. No. 2.1e-31; Matches 98; Conservative 37; Mismatches 66; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 50, Application US/10171311; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schlegel, Robert
; ORGANISM: Homo sapiens
US-10-138-787-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-50
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GENERAL INFORMATION:
APPLICANT: HOLIBING, Sacha
APPLICANT: PAWSON, TONY
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION: TYROSINE KINASES
FILE REPRESENCE: 11757_23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: OF/700473
PRIOR APPLICATION NUMBER: Of/021,272
PRIOR APPLICATION NUMBER: Of/021,272
PRIOR APPLICATION NUMBER: Of/021,272
PRIOR APPLICATION NUMBER: Of/021,272
SPRIOR APPLICATION NUMBER: Of/021,272
SPRIOR FILING DATE: 1996-07-05
SEQ ID NOS: 13
LENGTH: 228
                                                                                         APPLICANT: Mbamalu, Garaldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, TON;
TITLE OF INVENTION: DICCOMERZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS
TOWNER TELLING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VOF: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.4%; Score 435; DB 6; Length 209; Best Local Similarity 50.5%; Pred. No. 1.7e-33; Matches 96; Conservative 25; Mismatches 47; Indels
                                                 Sequence 6, Application US/10138787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-10-138-787-6
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173 LYEAPEPIFT 182
                     US-10-138-787-6
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Gerritsen, Mary E.
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APPLICANT:
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APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION: TYROSINE KINASES
FILE REPERBERCE: 1175-2305W0
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: DCT/CA97/00473
PRIOR APPLICATION NUMBER: DCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR APPLICATION NUMBER: 60/021,272
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
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138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                 120 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS------PQAHVNPQEKRLAADD 170
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                                                                                          198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
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                                                                                                                                                                    US-10-138-787-10
Sequence 10, Application US/10138787
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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Best Local S
Matches 87
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APPLICANT:
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APPLICANT: YUMBA DATIOL
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemil
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RLG331
CURRENT APPLICATION NUMBER: PCT/US02/24563
FURENT PILING DATE: 1907-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR PR
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40.9%; Pred. No. 5.2e-28;
iive 20; Mismatches 78
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Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Matches 85; Conserv
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ORGANISM: HOMO
PCT-US02-24563-288
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Conservative
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                                                     ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-050-288
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US-10-121-053-288
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Best Local Similarity
Matches 85; Conserva
SEQ ID NO 288
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LENGTH: 204
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                                                                       APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Steven
APPLICANT: Steven
APPLICANT: Tumathy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Anany, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330RL017
CURRENT APPLICATION NUMBER: US/10/121, 049
CURRENT APPLICATION TEMORY OF SECULO APPLICATION A
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1620
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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40.9%; Pred. No. 5.2e-28;
Live 20; Mismatches 78;
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Smith, Victoria
Stewart, Timothy A.
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Goddard, Audrey
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Gurney, Austin L.
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Watanabe, Colin K
Wood, William
                       Godowski, Paul J. Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 40.9%
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapien
US-10-121-049-288
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                         60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118
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  Length 204;
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CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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40.9%; Pred. No. 5.2e-28;
ive 20; Mismatches 78;
29.0%; Score 377.5; DB 6; 40.9%; Pred. No. 5.2e-28; ive 20; Mismatches 78;
    DB 6;
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Smith, Victoria
                       Best Local Similarity 40.9
Matches 85; Conservative
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RICS
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                            Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 377.5; DB 6;
Pred. No. 5.2e-28;
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Conservative 20;
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Stewart, Timothy A.
                                                                                                                                                         Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
                                                                               Gerritsen, Mary E.
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Gerritsen, Mary E.
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Watanabe, Colin K
Wood, William
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DeForge, Laura
                                                                                                                    Godowski, Paul J.
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Filvaroff, Ellen
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                                                                                                  Goddard, Audrey
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                                                               Gao, Wei-Qiang
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Best Local Simi
Matches 85;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C15
60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118
                                                             79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
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                                      138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
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CURRENT FILING DATE: 2002-04-12
Prior Application removed · See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
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                                                                                                                                                                                                                                                     Sequence 288, Application US/10121043
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Goddard, Audrey
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Wood, William
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Beresini, Maureen
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Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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Best Local Similarity 40.9°
Matches 85; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                    SULT 10
-10-121-043-288
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APPLICANT:
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Length 204; Indels 9

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60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118
                                                     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
     ; Sequence 288, Application US/10121056; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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DeForge, Laura
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Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood, William
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; ORGANISM: Homo Sapien
US-10-121-056-288
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C14
CURRENT APPLICATION NUMBER: US/10/121,054
CURRENT FILING DATE: 2002-04.12
                                                                                                                                                                                                                                                                                                                                                                   60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118
                                                                                                                                                                                                                                                                                                                                               79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                                138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                         119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS------PQAHDNPQEKRLAADD 169
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                                                                                                                                                                                                                                                                                               7 PLIGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA----- 59
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                                                                                                                                                                                                       Length 204;
                                                                                                                                                                                                                                            Indels
                                                    Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                           78;
                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                       29.0%; Score 377.5; DB 6
40.9%; Pred. No. 5.2e-28;
:1ve 20; Mismatches 78
FILE REFERENCE: P3330R1C4
CURRENT APPLICATION NUMBER: US/10/121,047
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PEVRVLHSIGHSAAPRL--FPLA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 FEGENPOVPKLEKSISGTSPKREHLPLA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerritsen, Mary E.
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DeForge, Laura
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Wood, William
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                                                                                                                                    ; ORGANISM: Homo Sapien
US-10-121-047-288
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; ORGANISM: Homo Sapien
US-10-121-054-288
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Best Local Similarity
Matches 85; Conserv
                                                                                                      LENGTH: 204
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APPLICANT:
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Matches 8
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C25
CURRENT APPLICATION NUMBER: US/10/121,056
138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                             60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118
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                                                                                                 198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                                                                                                                               198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
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RESULT

19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78

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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumax, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: ADANG, SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCENETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R[c13]
CURRENT APPLICATION NUMBER: US/10/121,057
CURRENT APPLICATION TEMOVEd - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
29.0%; Score 377.5; DB 6; Length 204;
Best Local Similarity 40.9%; Pred. No. 5.2e-28;
Matches 85; Conservative 20; Mismatches 78; Indels 25
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170 ----PEVRVLHSIGHSAAPRL--FPLA 190
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Sequence 288, Application US/10121057
GENERAL INFORMATION:
PPPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                        Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                  Gerritsen, Mary E.
Goddard, Audrey
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                                                                                                                                                                                                                                                                         Gurney, Austin I
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; ORGANISM: Homo Sapien
US-10-121-057-288
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APPLICANT:
APPLICANT:
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Search completed: September 28, 2002, 01:45:54 Job time: 619 sec

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September 28, 2002, 00:26:55; Search time 49.23 Seconds (without alignments) 464.539 Million cell updates/sec US-09-904-954-2 1301 1 MAAAPLLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Run on:

283138 Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	LERK-3 - human ELF-1 protein prec ephrin-A2 - human LERK-7 precursor - repulsive axon gui B61 protein precur LERK-4 - human hepatcma transmemb hepatcma transmemb hepatcma transmemb elk ligand - human hypothetical prote Stral/Epl92 protei LERK 2 - rat hypothetical prote prome polyprotein beta-D-galactosida hypothetical prote	
SUMMARIES	A54984 A54984 A54984 A563170 A57084 A57084 A65317 A65317 A65317 A65317 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A669993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A66993 A669	A48830 A75132 I50620
DB	000000000000000000000000000000000000000	1000
% Query Match Length	238 2193 228 228 228 336 346 346 201 1024 1024 1024 488 488 488 488 488 488 488 488 488 4	728 1144 1173
% Query Match	0.000	
Score	1301 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	82 82 81.5
Result No.	22222222222222222222222222222222222222	27 28 29

A54984
BLF-1 protein precursor - mouse
BLF-1 protein precursor - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: A64984 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
C.Accession: A54984, B.S.
R.Cheng, H.J.; Flanagan, J.G.
Ceil 79, 157-168, 1994

hypothetical prote protein BRG1 - hum	alkaline phosphata reversed polarity	env polyprotein pr phytocyanin At2g44	probable procein w beta-galactosidase hypothetical prote	transcription fact chitinase (EC 3.2.	genome polyprotein genome polyprotein	thermopsin precurs
T19109 S39059	545252 B72410 A54282	VCLJMN T01605	B84/89 GBEC T13389	I38238 S05426 A32392	GNNY4P S03822	н90370
200	700	777	7 11 7	2 1 2	7 7	7
457	104/ 434 612	859 202	498 1024 1291	321 328 700	2206	570
6.2	6.1	6.0	0.09	000	90.0	0.9
81	79.5 79	78.5	78.5 78.5	78 78 78	78	77.5
30	33 4 4	32 34 34	38 39	4 4 4 1 7 2	444	45

ALIGNMENTS

RESULT 138849 15886-3 C; Speci C; Dateci C; Acces R; Kozl N; Rozl A; Till A; Refec A; Refec A	RESGLT 1 LIERK-3 - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999 C; Accession: 138849 C; Accession: 138849 A; Ritle: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en A; Reference number: 138849; MUID:95140419 A; Reterence number: 138849; MUID:95140419 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Cross-references: EMBL:U14187; NID:9642832; PIDN:AAC50078.1; PID:9642833 A; Cross-references: GDB:438336; OMIM:601381 A; Map position: 1q21-1q22 C; Superfamily: axon guidance signal protein
Que Bes Mat	Query Match Best Local Similarity 100.0%; Score 1301; DB 2; Length 238; Best Local Similarity 100.0%; Pred. No. 1.7e-114; Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MAAAPLILLILIVPVPLLPLAQGPGGALGNRHAVYMNSSNOHLRREGYTVOVNVNDYLD 60
Dp	
Qy	61 IYCPHYNSSGVGPGAGPGPGGAEQYVLZMVSRNGYRTCNASOGFKRWECNRPHAPHSPI 120
Qy	121 KFSEKFQRYSAFSLGYEFHAGHEYYXISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
Db	
Qy	181 LPQFTWGPNYKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLWTFLAS 238
Db	

a

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Query Match 31.9%
Best Local Similarity 39.5%
Matches 98; Conservative
                                            171 SHSGEKPVPT 180
                                                                                 177 LYEAPEPIFT 186
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|LEFLLAML 225
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    117
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A:Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the A:Reference number: A54984; MUID:95007776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                huma
                                 A. Accession: A54884
A. Status: preliminary
A. Molecule: type: mRNA
A. Residues: 1-209
A. CHES
A. Cross-references: GB:U14941; NID:9558836; PIDN:AAA53636.1; PID:9558837
A. Cross-references: GB:U14941; NID:9558836; PIDN:AAA53636.1; PID:9558837
B. Shao, H.; Lou, L.; Panday, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
B. Fishio, H.; Lou, L.; Panday, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
A. Reference number: A55873; MUID:95181289
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-209
A. SHAA
A. Residues: 1-209
A. Cross-references: GB:U14752; NID:9681886; PIDN:AAA68520.1; PID:9681887
C. Superfamily: axon guidance signal protein
C. Keywords: lipoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
Biochen. Biochen. Res. Commun. 252, 378-382, 1998
A; Tille: Cloning, chromosal mapping, and tissue expression of the gene encoding the
A; Reference number: JE0322; MUID:99045414
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A; Status: preliminary
A; Molecule type: many
A; Residues: 1-213 cAAS
A; Residues: 1-213 cAAS
A; Cross-references: GB: AJ007292; NID: g3688367; PIDN: CAA07435.1; PID: g3688368
C; Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Species: Homo sapiens (man)
'Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
'Accession: JE0322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINDYLDIYCPHY-----GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AQRPLLPLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV
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Pred. No. 3.2e-33;
1; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 437; DB 2;
Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                          33.6%; Scor.
50.5%; Pred. No. ....
'... 25; Mismatches
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50.5%; Pred
tive 24; J
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Best Local Similarity 50.5'
Matches 96; Conservative
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Best Local Similarity
Matches 96; Conserv
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C; Species: Homo saples (man)
C; Date: 00-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C; Accession: 158170; G01812
R; Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.
A; Title: (Loning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involv
A; Reference number: 158170; MUD: 95267434
A; Accession: 158170
A; Accession: 158170
A; Residues: 1-228 (RES)
A; Residues: Carretti, D.P.; Carpenter, M.K.
Submitted to the EMBL Data Library, May 1995
A; Reference number: G08477
A; Molecule type: mRNA
A; Residues: 1-228 (ROS)
A; Rosidues: 1-228 (ROS)
A; ROSIDUE A; ROS
A; ROSIDUE 
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PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A,Cross-references: GDB:568757; OMIM:601535
A,RMap Dostition: 13q33-13q33
C,Superfamily: axon guidance signal protein
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Sep

Sur

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Gaps

13;

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 14-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C; Accession: 184743
R; Bennett, B.D; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matth Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A; Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine A; Accession: 184743
A; Accession: 184743
A; Accession: 184743
A; Molecule type: mRNA
A; Residues: 1-333 < RES
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs A;Reference number: 138849; MUID:95140419
A;Accession: 138850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <RES>
A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
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C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 364.5; DB
Pred. No. 9.9e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 0%; Score 44.5%; Pred. No. 2007.
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C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                              OMIM: 601380
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                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 13q33-13q33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB: EPLG5; LERK5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
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Best Local S
Matches 77
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bill protein precursor - human C; Species: Homos sapiens (man) C; Decies: Homo sapiens (man) C; Decies: Homo sapiens (man) C; Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999 C; Accession: A36377 R; Holzman, L.B.; Marks, R.M.; Dixit, V.M. Mal. Cell. Biol. 10, 5830-5838, 1990 A; Fitle: A novel immediate-early response gene of endothelium is induced by cytokines in A; Recession: A36377; MuID:91042512 A; Recession: A36377; MuID:91042512 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-205 CHOL> A; Residues: 1-205 CHOL> A; Cross-references: GB:M57730; GB:M37476; NID:9179320; PIDN:AAA58388.1; PID:9179321 C; Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 FKEGHSYYXISKPIHQHEDRCLRLKVTV-SGKITHS------PQAHVNPQEKRLAADD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                               8 LILLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 390; DB 2; Length 20
41.8%; Pred. No. 4.1e-29;
ive 21; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.1%; Score 404.5; DB 2;
49.1%; Pred. No. 2e-30;
tive 29; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PEVRVLHSIGHSAAPRL--FPLA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEGENPOVPKLEKSISGTSPKREHLPLA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 41.8 nes 87; Conservative
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.1:
Matches 79; Conservative
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Best Local S
Matches 87,
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                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
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7;

Gaps

us-09-904-954-2.rpr

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Strai/Fepig2 protein - mouse
C; Species: Mis musculus (house mouse)
C; Species: Mis musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: I48780; A55507; A5562; S25670
R; Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Doll Dev. Biol. 170, 420-433, 1995
A.Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona A; Reference number: I48780
A; Accession: I48780
A; Accession: I48780
A; Accession: I48780
A; Residues: 1-345 < REES
A; Cross-references: EMBL: 248781; NID:g747858; PIDN: CAA88695.1; PID:g747859
R; Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A Genomics 24, 127-132, 1994
A; Title: Genomic organization and chromosomal localization of mouse Epig2, a gene enc A; Reference number: A55507; MuID:95203867
A; Accession: A55507
A; Accession: A55507
A; Accession: A55507
                                                                                                                                                                                                                                                                  hypochetical protein F56All.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Qaenorlabditis elegans
C;Species: 129-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32645
R;Gattung, S; Goela, D; Harper, M.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F56All.
A;Reference number: 221204
A;Reference number: 221204
A;Reference number: 221204
A;Reference number: 221204
A;Residues: 17462
A;Katus: prellminary; translated from GB/EMBL/DDBJ
A;Residues: 11462 <ART>
A;Residues: 31462 <ART>
A;Residues: 31462 <ART>
A;Residues: 31462 <ART>
A;Residues: 31463 <ART>
A;Residues: 31463 <ART>
A;Residues: 31463 <ART>
A;Resperimental source: strain Bristol N2; clone F56All
A;Agene: CESP:F56All.3
A;Agene: CESP:F56All.3
A;Adp position: 4
A;Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 FSEKFQRYSAFSLGYEFHAGHEYYYISTPT-----HNLHWKC-----LRMKVFVCCA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 LIVYEVTEFAMDDCALESHSREVIRCAPEGTAEKVLRTQQLSGGRREDWKKQKVP--PKN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 STSHSGEKPVPTLPQFTMGPNVKINVL---EDFEGENPQVPKLEKSISG-TSPK 218
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Llarity 23.1%; Pred. No. 1.5e-05;
Conservative 30; Mismatches 93
                                              189 NVKINVLEDFEGENPQVPKLEKSISGTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 54; Conserv
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A;Molecule type: DNA
A;Residues: 1-345 <FLE>
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                                                       hepstoma transmembrane kinase ligand - mouse (5 Species: Mus musculus (house mouse) (5 Species: Mus musculus (house mouse) (5 Species: 02-301-1996 #sequence_revision 02-301-1996 #text_change 05-Nov-1999 (5 Accession: 149766 #sequence_revision 02-301-1996 #text_change 05-Nov-1999 (5 Accession: 149766 #sequence_revision 02-301-1996 #text_change 05-Nov-1999 (5 Accession: 149766 #sequence_revision 02-301-1995 #sequence_revision of a ligand for the EPH-related receptor protein-tyrosine kin A. Accession: 149766 #sequence number: 149766 #sequence 
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C;Date: 15-U1-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C;Date: 15-U1-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C;Accession: $46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlc EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kind A;Reference number: $46993; MUID:94349923
A;Accession: $46993
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 DOADRCTIKKENTPLLNCAR---PDQDVKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLH-------WKCLRMKVFVCC---ASTSHSGEKPVPT-LPQFTMGPNVKINVLEDFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 MVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 TPTHNLH-------WKCLRMKVFVCCA------STSHSGEKPVPTLPQFTMGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| : | : | | : | | 137 TSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQAP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 NRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-336 <RES>
A; Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 171.5; DB 2; 28.3%; Pred. No. 2.4e-08; tive 27; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 148.5; DB 2; 26.4%; Pred. No. 3.5e-06; tive 26; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 GENPQVPKLEKSI -- SGTSPKREHLPLAVGIAFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 KPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFI 242
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Best Local Similarity 26.4%
Matches 55; Conservative
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Best Local Similarity 28.3%
Matches 62; Conservative
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A; Residues: 1-346 <BEC>
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Nicontains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c A-directed RNA polymerase (EC 2.7.7.48)
Adirected RNA polymerase (EC 2.7.7.48)
C; Species: human poliovirus 3
C; Species: human poliovirus 3
C; Accession: A27245
R; Hughes, P.-J.; Evans, D.M.A.; Minor, P.D.; Schild, G.C.; Almond, J.W.; Stanway, G. A; Ritle: The nucleotide sequence of a type 3 poliovirus isolated during a recent outb A; Reference number: A27245; MUD: 87010550
A; Ritle: The nucleotide sequence of a type 3 poliovirus isolated during a recent outb A; Reference number: A27245; MUD: 87010550
A; Rocession: A27245
A; Molecule type: genomic RNA
A; Residues: 1-2206 < HUGS
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A; Cross-references: GB:X04468; NID:g61112; PIDN:CAA28155.1; PID:g61113
C; Superfamily: poliovirus genome polyprotein
C; Superfamily: poliovirus genome protein; genome-linked protein; nucleotidyltransferase
F; 1-69/Product: coat protein VP4 #status predicted <VP4>
F; 70-340/Product: coat protein VP3 #status predicted <VP3>
F; 579-878/Product: coat protein VP1 #status predicted <VP3>
F; 579-878/Product: coat protein VP1 #status predicted <VP3>
F; 879-1027/Product: core protein P2-3b #status predicted <P3B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-356 <LYN>A;Cross-references: EMBL:AL031854; PIDN:CAA21282.1; GSPDB:GN00067; SPDB:SPBC337.12
A;Experimental source: strain 972h-; cosmid c337
                                                                                                                                                                                                                                                                                                                                                                hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Sacession: T40265
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, October 1998
A;Rocession: T40265
A;Rocession: T40265
A;Accession: T40265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 LYWNNKSYLLKKKRFLKEVG-NSPSAVYCRYYNANGI------CGKGAACRFVHEPTRK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 TICPKFLNGRCNKAEDCNLSHELDPRRIPACRYFLLGKCNNPNCRYVHIHYSENAPICFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NGYRTCN------ASQGFKRWECNRPHAPHSPIKFSE-----K 125
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          ---STSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPOVPKLEK
                                            84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 FAKYGFCELG-----TSCKNQHILQCTDYAMFGSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 TMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLA 225
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Pred. No. 0.13;
1; Mismatches
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19.0%; Pred
31;
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SPDB:SPBC337.12
          162 KVFVCCA-
                                                                                                                                      211 SISG 214
                                                                                                                                                                                                        217 SGPG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                        for the Cek5 receptor protein-tyd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: 158406 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: 15840, 1994
A;Fitle: LERR-2, a ligand for the receptor tyrosine kinase ELK, is evolution A;Reference number: 158406; MUID:95022634
A;Reference number: 158406
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SRNGYRTCNASQGFKRWEC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 CPHYNSSGVGPGAGPGGGAEQYVLYMV-----SRNGYRTCNASQGFKRWEC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KPHQEIRFTIKFQEFSPNYMGLEFKKYHDYXIISTSNGSLEGLENREGGVCRTRTM 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 KVFVCCA-----STSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 KIVMKVGQDPNAVTPEQLITSRPSKESDNTVKTATQAPG--RGSQGDSDGKHETVNQEEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 NRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLH-------WKCLRM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 NRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLH------WKCLRM 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AMVVLTLCRLATPLAK------NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 APLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIY 62
R; Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.

J. Biol. Chem. 269, 26606-26609, 1994

A; Title: cDNA cloning and characterization of a ligand for the Cek5 recep

A; Reference number: A55062; MUID:95014510

A; Recession: A55062

A; Status: preliminary; not compared with conceptual translation

A; Residues: 1-89, 'T', 91-345 <SHA>

A; Cross-references: GB:U12983; NID:9575928; PIDN:AAA53231.1; PID:9575929

C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 139.5; DB 2; 24.2%; Pred. No. 2.4e-05; ive 27; Mismatches 87;
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Matches 59; Conservative
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A; Residues: 1-345 <RES>
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Best Local Simil
Matches 58; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 SHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQ-----VPKLEKSISGTSPKREHLP- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 TLDTVMMGKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQ------CNASK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSTINYTINYYKDSASNAASKQDYSQDPSKFTEPLKDVLIKTAPALNSPNV----- 73
                                                                                                                                                                                                                                                                                                                                                                          26 GGALGNRHAV--YWNSSNQHLRREGYTVQVN----VNDYLDIYCPHYNSSGVGPGAGPG 78
F;1028-1124/Product: core protein P2-5b #status predicted <P5B>
F;1125-1453/Product: core protein P2-X #status predicted <P2X>
F;11454-1540/Product: protein P3-1b #status predicted <P1B>
F;1541-1562/Product: genome-linked protein VPG #status predicted <VPG>
F;1541-1562/Product: proteinsse #status predicted <PTS>
F;1563-1745/Product: RNA-directed RNA polymerase #status predicted <RNS>
F;1746-2206/Product: RNA-directed RNA polymerase #status predicted <RNS>
F;1543/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                           Query Match 7.0%; Score 91; DB 1; Length 2206; Best Local Similarity 20.5%; Pred. No. 8.1; Matches 52; Conservative 29; Mismatches 109; Indels
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Search completed: September 28, 2002, 01:38:54 Job time: 4319 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                  OM protein - protein search, using sw model
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September 28, 2002, 01:37:46; Search time 27.02 Seconds (without alignments) 341.053 Million cell updates/sec US-09-904-954-2 1301 1 MARAPLILLILLVPVPLLPL.....REHLPLAVGIAFFLMTFLAS 238 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P52797 homo sapien O08545 mus musculu	m snm	_ ·	P/9/2/ brachydanio	P52802 garras garr P52803 homo sapien	mus m	P97605 rattus norv		-	_			P52793 mus musculu	. P52798 homo sapien	P97553 rattus norv	Q15768 homo sapien	mus n	P52799 homo sapien	mus m	P98172 homo sapien	bracl		O13097 xenopus lae	G	_		Q12906 h interleuk	3 mu	Q9jil3 rattus norv	_	P07247 drosophila
	EFA3_HUMAN EFA3_MOUSE	EFA2_MOUSE	- 1	EFAZ_BRARE	EFAS_HUMAN	EFA5_MOUSE	EFA5_RAT	EFA4_MOUSE		EFA5_BRARE		EFA1_XENLA	EFA1_MOUSE	EFA4_HUMAN	EFA1_RAT	EFB3_HUMAN	EFB3_MOUSE	EFB2_HUMAN	EFB2_MOUSE	EFB1_HUMAN	EFB2_BRARE		EFB1_XENLA	EFB1_RAT		POLG_POL32	ILF3_HUMAN		ILF3_RAT	ENV2_MOUSE	KRUP_DROME
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% Query Match Len	00	33.6	33.6	32./			31.9	31.5	31.1	30.5	30.0	28.9	28.7	28.0	27.8	13.8	13.6	13.2	13.2	11.4	11.3	10.7	10.3	10.2	4.	0.	8.9	6.5	6.4	6.3	6.3
Score	1301 963	437	437	420	415.5	414.5	414.5	410	404.5	397	390	375.5	374	364.5	362	179	177	171.5	171.5	148.5	147	139.5	134	32		91	88.5	æ	83.5	ď	82.5
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	Q9z1x4 mus musculu P51532 homo sapien						
SOX2_MOUSE CAHX_CAEEL	ILF3_MOUSE SN24_HUMAN	ROG_HUMAN ENV HV1MN	BGAL_ECOLI	SOX2_HUMAN	SOX2_SHEEP	CHIT_SOLTU	KPC2_DROME
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6.3	6.2	6.1	0.9	9.0	6.0	0.9	0.9
82 82	81 81	79.5	78.5	78	78	78	78
34 35	36 37	38 39	40	47	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFA3_MOUSE STANDARD; PRT; 187 AA.
00845; 055217;
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last enceptor tyrosine kinase ligand 3) (LERK-3)
EPHILD-A3 (EPHILL) (Fragment).
EPHA3 OR EPLG3 OR LERK3 OR EPLA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98126446; PubMed-9465306;
Cerrettl D.P., Nelson N.;
"Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
conservation of intron/exon structure.";
                                                                                                                                                                                                                                                                                                                                                     MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
        (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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MEDLINE-97060319; Pubmed-8903354;
Fleniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for "Distinct and Overlapping expression patterns" and Distinct and Overlapping expression patterns of Distinct and Overlapping expression patterns of Distinct and Distinc
  N-LINKED (GLCNAC. ..) (POT)
N-LINKED (GLCNAC. ..) (POT)
N-LINKED (GLCNAC. ..) (POT)
MISSING (IN REF. 2).
W; BEFDGAE8FE33FDDA CRC64;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                        100.0%; Score 1301; DB 1;
llarity 100.0%; Pred. No. 2.8e-115;
Conservative 0; Mismatches 0;
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     38
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71
238 AA;
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                                                                                                                                                                                                                                                                 Matches 238;
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                                                           CARBOHYD
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Best Local 3
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EFA3_MOUSE
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                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                          104 GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKV
                                                                                                                                                                                                                                                                                        FVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed
                                                         (POTENTIAL). (POTENTIAL). (POTENTIAL).
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01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (ELF-1) (CEKY-11gand) (CEK7-L).
EFNAZ OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
                                                                                                                                                                                                      ..
80
                                                                                                                                                                            Length 187;
                                                                                                                                                                  Score 963; DB 1; Length 10
Pred. No. 1.3e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SWISS WEBSTER; TISSUE-Brain; MEDLINE-95007776; PubMed-7522971; Cheng H.J., Flanagan J.G.; "Identification and cloning of ELF-1, a developmentally eligand for the Mek4 and Sek receptor tyrosine kinases."; Cell 79:157-168(1994).
                                                                                                                               -> W (IN REF. 2).
CCE4915751760743 CRC64;
                                                      N-LINKED (GLCNAC. ..) (F
N-LINKED (GLCNAC. ..) (F
N-LINKED (GLCNAC. ..) (F
Y > 1 (IN REF. 2).
EQ -> DR (IN REF. 2).
RT -> QP (IN REF. 2).
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                                              74.0%;
91.3%;
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41
49
19
34
47
78
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin;
PROSITE; PS01299; EPHRIN;
Glycoprotein; GPI-anchor.
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41
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78
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P52801;
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                                                                                                                                                                                                                                                                                                              Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.; "Cloning, chromosal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2."; Blochem. Biophys. Res. Commun. 252:378-382(1998).
   Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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N-LINKED (GLCNAC. . ) (POTE
N-LINKED (GLCNAC. . ) (POTE
R -> A (IN REF. 3).
RA -> PP (IN REF. 3).
AA -> RR (IN REF. 3).
                                                                                                                                                            Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
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EMBL; U92894; AAC39577.1; JOINED.
EMBL; W02894; AAC39577.1; JOINED.
EMBL; AC004258; AAC4896.1; --
EMBL; AJC073292; CAAC7435.1; --
INIM; 602756; --
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                     MEDLINE-99045414; PubMed-9826538;
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PRINTS; PR01347; EPHRIN.
PROSTE; P801253; Ephrin; 1.
PROSTE; P801299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Sign SIGNAL
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213 AA;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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42
174
188
                                                                                                                               Carrano A.V.;
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SEQUENCE FROM N.A.

CETTELLID.P., Nelson N.;

"Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),

"Characterization of the genes for mouse LERK-6/Ephrin-A2 (Epl6):

CONSELVATION OF INTRON/EXON STRUCTURE.";

Genomics 47:131-135(1998).
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Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAAPLLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-----GYTVQV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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15-DEC-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-DEPALIN-25 precursor (EPH-related receptor tyrosine kinase ligand
(LERK-6) (HEK7-119and) (HEK7-L).
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F1997545F25B9ABC CRC64;
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SIGNAL 1 20 POTE
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EMBL; U14752; AAA68220.1; --
MGD; MGI:102707; Efna2.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin.
Probom; P0002533; Ephrin.
PROSITE; PS01299; EPHRIN.
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ID EFA2_H

AC 03921

DT 15-DEC

DT 15-DEC

DE EPHTIN

DE EPHTIN

DE EFREX

OC ENKARY

OC ENTARY

ENT (2)

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Gaps

18;

(POTENTIAL).

63

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EFA2_CHICK
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                              EFA2_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                        -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF DEVELOPING BRARYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADED FASHION THROUGHOUT THE TECTUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
SIGNAL 1 16 POTENTIAL.
CHAIN 17 195 EPHRIN-A2.
                                                                                                                                                                                                                                                                                                         Development 124:655-664(1997).
-1- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                                                     may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FWVNHDGYLTCEHRMRGFKRWECNRPQSPDGPLRFSEKFQLFTPFSLGFEFRPGHEYYI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 YMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 ISDRHAVYWNSSNSRFWQGEYTVAVSINDYLDVYCPYYES------PQPHSRMERYIL 74
                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
(LERK-6) (ELF-1) (2FPHL3).
EFNA2 OR EPLG6 OR LERK6.
                                                                                                       Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Exfinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cyptiniformes; Cyptinidae; Danio.

    SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor

                                                                                                                                                                                                                                      Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U., abohoeffer F., Holder N.; "Two Eph receptor tyrosine kinase ligands control axon growth and be involved in the creation of the retinotectal map in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL). 9EE284FEB61D0C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                           -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.7%; Score 426; DB 1; Length 195; 52.3%; Pred. No. 4.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 SSPHPNHAGKPCLKLKVYV--KPTSSGYESPEPFL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 STPTHNLHWK-CLRMKVFVCCASTSHSGEKPVPTL 181
 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y09668; CAA70863.1; -. ZFIN; ZDB-GENE-990415-66; efna2. InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRNTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                         MEDLINE-97195707; PubMed-9043080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 N-
22688 MW;
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
EFA2_BRARE
P79727;
                                                                                                                                                                                                                                                                                               zebrafish.
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                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CPHYEE-----PLPAERMERYVLYMVNYECHASCDHRQKGFKRWECNRPDSPSGPLK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 82:371-381(1995)
--- SUBUNTH: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3; EPHA4 AND EPHA5 (BY SIMILARITY)
--- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
"Complementary gradients in expression and binding of ELF-1 and Mek4
in development of the topographic retinotectal projection map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AAPLILLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
                                                                                                                                                                          Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (ELF-1).
EFNA2 OR EPLG6 OR LERK6 OR ELF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8FAB1AESE45EED96 CRC64;
                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
EPHRIN-A2.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-95360981; Pubmed-7634327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L40932; AAC42229.1; -. InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; GPI-anchor; SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002533; Ephrin; PROSITE; PS01299; EPHRIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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VARIANT
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EFA5_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        es Dev. 13:3125-3135 (1999).

FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

BUNDES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE

MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS

COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF

THE FYN TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                         Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.,
"LERK-7: a ligand of the Eph-related kinases is developmentally
regulated in the brain.";
Cytokine 9:540-549(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin, 1.
PRINTS; PR01347; EPHRIN.
ProDom; P0002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ephrin-A5 requires the
                                                                                                                                                                                                                                                                  Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C., Staal S.P., Goddard A., Henzel W.J., Heffil F.; "Cloning of AL-1, a ligand for an Ephrzelated tyrosine kinase receptor involved in axon bundle formation.";
                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-A5.
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davy A., Gale N.W., Murray E.W., Klinghoffer R.A., Soriano P., Feuerstein C., Robbins S.M.; "Compartmentalized signaling by GPI-anchored ephrin-A5 requires. Fyn tyrosine kinase to regulate cellular adhesion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20069483; PubMed-10601038;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-95267434; PubMed-7748564;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97392664; PubMed=9245480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U26403; AAB60377.1; -.
                                                                                                                                               (LERK-7) (AL-1).
EFNAS OR EPLG7 OR LERK7.
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                        Neuron 14:973-981(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
228
37
                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICRODOMAINS
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
21
37
                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism
                                                                EFA5_HUMAN P52803;
173 T 173
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes
                                                   EFA5_HUMAN
                                       RESULT
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                                                                                                                                                                                                                                                11;
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"Distinct and overlapping expression patterns of ligands for
"Distinct and overlapping expression patterns of ligands for
Eph-related receptor Lyrosine Kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).

-I- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEDAE-LIKE
MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
THE FYN TYROSINE KINASE (BY SIMILARITY).

-I- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
EPHBI (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 EDS------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                         99
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                                                                                                                                                                                                                                                                                                                         LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                             ( MLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI-----PSR-----LLAI
                                                                                                                                                                                                                                                47;
                                                                                                                                                                              Length 228;
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                                                                                                                                                                                                                                                Indels
                                    /FTId=VAR_012035.
6893B1CCACFF3F57 CRC64;
N -> K (IN DBSNP:469062).
                                                                                                                                                                       ; Score 415.5; DB 1;
; Pred. No. 5.7e-32;
37; Mismatches 66;
                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFA5_MOUSE STANDARD; PRT; 228 AA. 008543; 008544; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-97060319; PubMed-8903354;
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EFNAS OR EPLG7 OR LERK7 OR EPL7.
                                                                        26297 MW;
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                                                                                                                                                                                                               Similarity 39.5
18; Conservative
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                                                                        228 AA;
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   55
                                                                                                                                                                Query Match
Best Local Simi
                                                                        SEQUENCE
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[1]
SEQUENCE FROM N.A.
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EMBL; U90665; AAB50239.1; -.
MGD; MGI:10744; Efnas.
InterPro; IPR001799; Ephrin.
Prints; PR01739; Ephrin. 1.
PRINTS; PR01737; EPHRIN.
ProDom; P0002533; Ephrin; 1.
PROSTTE; PS01299; EPHRIN. 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal; Alternative splicing.
SIGNAL 1 20 POTENTIAL.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
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"ILEBRY, rat ligand for Eph-related receptor tyrosine kinase.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Ephinn-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LPQFTMGPNVKINVLEDFE-----GEN-PQVPKLEKSISGTSPKREHLPLAVGI
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N-LINKED (G.CNAC. ..) (POTENTIAL).
MASSING (IN SHORT ISOFORM).
85439F5337420022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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163 189 M
228 AA; 26339 MW;
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EFNAS OR EPLG7 OR LERK7.
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VARSPLIC
SEQUENCE
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MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).
                                                                                            -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 EDS------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              008542; 055218;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand
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855985532D580022 CRC64;
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39.5%; Pred. No. 7.1e-32;
iive 36; Mismatches 67;
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InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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228 AA; 26358 MW;
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Best Local Similarity 39.5%
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EDS------VPEDKTERYVLYMVNPDGYSSCDHISKGFKRWECNRPHSPNGPLKFSEK 117
                                             Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                         Cell 82:359-370(1995).
-!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL GANGLION CELL AXONS.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LLLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LERK-7) (AL-1) (ZFEPHL4).
EFNAS OR EFNASB OR ALI OR EPLG7 OR LERK7.
Brachydanio retaio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL) 56D8E4FBDECF18AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.1%; Score 404.5; DB 1; Length 228; 49.1%; Pred. No. 6.2e-31; Indels 11
                                                                                                                                                                                                Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda Bonhoeffer F.,
                                                                                                                                                                                                                                         "In vitro guidance of retinal ganglion cell axons by RAGS, a tectal protein related to ligands for Eph receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                       TISSUE=Posterior tectum;
MEDLINE=95360980; PubMed=7634326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA; 26206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; IPRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X90377; CAA62027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sim-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFA5_BRARE
P79728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
EFA5_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     э;
                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrlin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
EFNAS OR RAGS.
                    Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.; "Distinct and overlapping expression patterns of ligands for Eph-related receptor tyrosine kinases during mouse embryogenesis."; Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EPHRIN-A4.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 IQRYTPFPLGFEFLPGETYYYISVPTPESPGRCLRLOVSVCCKESGSSHESAHPV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%; Score 410; DB 1; Length 206; 47.4%; Pred. No. 1.7e-31; Live 18; Mismatches 62; Indels
                                                                                                                                                                                         Cerretti D.P., Nelson N.; "Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Ep14), and human LERK-6/Ephrin-A2 conservation of intron/exon structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43501971DD1C6EA5 CRC64;
                                                                                                                                                                                                                                                                                                                              similarity).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 AA
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                                                                                                                                                                           MEDLINE-98126446; PubMed-9465306;
MEDLINE=97060319; PubMed=8903354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U92889; AAC39962.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22861 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U90663; AAB50238.1; -. EMBL; U92890; AAC39962.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                    Genomics 47:131-135(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; GPI-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 83; Conserv
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFA5_CHICK
P52804;
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EFA5_CHICK
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GPI-ANCHOR
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ς.
Έ
                                                                                                                                                               Development 124:655-664(1997).
-!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
                                                                                                                           тау
                                                                                                                                                                                                                 (POLENTIAL).
-1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE
TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 NSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 EDS------VPEERTERYVLYWVWYDGYSTCDHTAKGFKRWECNRPHSPNGPLKFSEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-RAR-2002 (Rel. 41, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (Immediate early response protein B61) (Tumor necrosis
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                            Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U., abnoheeffer F., Holder N.; "Two Eph receptor tyrosine kinase ligands control axon growth and be involved in the creation of the retinotectal map in the
                                                                                                                                                                                                        SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LLLLVPVPL-LPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL) 74B3406C05418E6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%; Score 397; DB 1; Length 228; 47.8%; Pred. No. 3.1e-30; Live 30; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :: ||||:|| | |||||| || FQLFTPFSLGFEFRPGREYYISSMITETGRRSCLKLKVFV 158
                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: Y09669; CAA70864.1; ...
ZFIN; ZDB-GENE-980526-186; efna5b.
InterPro: IPR001799; Ephrin.
Pfam; PP00812; Ephrin. 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                  TISSUE-Embryo;
MEDLINE-97195707; PubMed-9043080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 AA; 26595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 47.8
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
228
37
                                                      SEQUENCE FROM N.A.
                           NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFA1_HUMAN P20827;
                                                                                                                                                       zebrafish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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EFA1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                           MEDLINE-91042512; PubMed-2233719;
Holzman L.B., Marks R.M., Dixit V.M.;
"A novel immediate-early response gene of endothelium is induced by cytokines and encodes a secreted protein.";
Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 PLIGLCCSLAAADRHIVFWNSSNPKFRNEDYTHYQLNDYVDIICPHYEDHSVADAA---
                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (1
4FEFC6BF4C1251A9 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 390; DB 1; L
41.8%; Pred. No. 1.3e-29;
Live 21; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 FEGENPOVPKLEKSISGTSPKREHLPLA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PEVRVLHSIGHSAAPRL--FPLA 191
factor, alpha-induced protein 4).
EFNA1 OR EPGL1 OR LERK1 OR TNFAIP4.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95140419; PubMed-7838529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PRO1347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 AA; 23771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M57730; AAA58388.1; -. PIR; A36377; A36377. MIM; 191164; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=9606;
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
TPPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC
TLYGLLLAALLIRL -> SE (IN ISOFORM A').
1B3A508E0A7B872E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97000306; Pubmed-8843391; Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A.; "Embryonic expression of eph signalling factors in Xenopus."; Mech. Dev. 57:133-144(1996).

-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4, EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 LYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQV- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ISKPIHYHGETCMRLRVHV-----SGRTTPPPVNVHTPRSHI------QSDEPEVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 AQGERHIVFWNSSNYRFWQEDYTVQVQLNDYLDIVCPYYEEGSVA-----GHTVERYT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYV 87
                                                                                                                                                      Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK-1) (XELF).
EFNAI OR EPGLI OR ELF.
                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.9%; Score 375.5; DB 1; Length 216; ilarity 41.1%; Pred. No. 3.1e-28; Conservative 25; Mismatches 63; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN-A1.
N-LINKED (GLCNAC.
                          P52794;
01-0cr-1996 (Rel. 34, Created)
10-Ccr-1996 (Rel. 34, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24755 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U31204; AAA74485.1; -. EMBL; U31205; AAA74486.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; GPI-anchor;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 -PKLEKSISGTS 216
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184 LPGVMKSVAGNS 195
                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'-hac 79; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
EFA1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFAL_MOUSE STANDARD; PRT; 205 AA.
P52793; P9731;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
EFNAL OR REPGIL OR LERKI OR EPLI).
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris J.C., Ciarletta A., Morris G.E., Giannotti J., Caruso A., Hammett D.J., Finnerty H., Turner K., Wood C.R.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                      Takahashi H., Ikeda T.; "Molecular cloning and expression of rat and mouse B61 gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-i- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) 
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EPHRIN-A1.
N-LINKED (G)
                                                                                                                                                                                                                                                                                                                                       STRAIN=ICR;
MEDLINE=95405853; PubMed=7675446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                     implications on organogenesis.";
Oncogene 11:879-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D38146; BAA07344.1; -.
EMBL; U26188; AAA67563.1; -.
EMBL; U90662; AAB50237.1; -.
MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO1347; EPHRIN.
ProDom: PRO02533; EPhrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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SEQUENCE FROM N.A.
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9
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                                                               Query Match 28.7%; Score 374; DB 1; Length 205; Best Local Similarity 38.7%; Pred. No. 4e-28; Matches 86; Conservative 23; Mismatches 87; Indels 26;
204 204 S -> T (IN REF. 1).
205 AA; 23802 MW; 5A8F3A6E2091E868 CRC64;
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Search completed: September 28, 2002, 01:48:24 Job time: 638 sec

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09r262 mus musculu 09z217 mus musculu 016783 caenorhabdi O9ykq4 human immun Q17657 caenorhabdi 005672 saccharomyc 0961a1 drosophila 007619 saccharomyc

090233 090423 090423 090423 090803 091201 091201 091201 091201 091201 091201 091202 092202 092202 092202 097604 001657

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September 28, 2002, 01:36:55; Search time 79.86 Seconds (without alignments) 515.562 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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1301
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_archeap:*

sp_vertebrate:*
sp_unclassified:*

sp_bacteriap:*

sp_rvirus:*

SUMMARIES

092394 rattus norv 098tz1 gallus gall 09ptd0 ctenophorus 09czs8 mus musculu 093431 brachydanio 09787 mus musculu 09we7 rattus norv 09ptd1 ctenophorus 042304 brachydanio 09cz13 mus musculu 09cz13 mus musculu 09cz3 brachydanio 09pt69 xenopus lae 09pt69 yenopus lae 09pt94 gallus gall Q90yc5 brachydanio Description 098TZI 098TZI 099TD0 093431 090TZI 090TZI 090ZZI 090ZZI 090ZZI 090ZZI Query Match Length DB 424.5 406 406 406 3373 367 3873 247.5 208 1186.5 1166.5 1165.5 Result Š.

RESULT 1 Q90YC5	Q90YC5 PRELIMINARY; PRT; 219 AA.			(TrEMBLrel, 19,	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	EPHRIN-A3.	EPHRIN-A3.	Brachydanio rerio (Zebrafish) (Zebra danio).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Cypriniformes; Cyprinidae; Danio.						"Identification of ephrin-A3 and novel genes specific to the midbrain-	MHB in embryonic zebrafish by ordered differential display.";		EMBL; ABO	
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Q9JIL3 Q9GPP6 Q9DIF1 Q9HBC3 Q13648

sp_fung1:*
sp_human:*
sp_invertebrate:*

sp_organelle:*

sp_phage:* sp_mhc:*

sp_mammal:*

sp_plant:* sp_rodent:*

sp_virus:*

09V9N4

Gaps 43; Indels 18; Length 219; Ouery Match 55.9%; Score 727; DB 13; Best Local Similarity 61.9%; Pred. No. 1.4e-67; Matches 140; Conservative 25; Mismatches 43;

3;

61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120 1 MAAAPLILILILIVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60 qq ŏ

KFSEKFORYSAFSLGYEFHAGHEYYXISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180 121

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91E2716FF91353F9 CRC64;

22624 MW;

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PS01299; EPHRIN; 1.
                            202 AA;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
EPHRIN-A6 (FRAGMENT).
EPHRIN-A6 (FRAGMENT).
EURATYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
105 KFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHHGRSCLRLRVYVCCSTASDSDDEPQPT 164
                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPIKF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 SEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.; "Ephrin A6, a new ligand for EphA receptors in the developing visual
                                                                                                                                                                                                                                                                                     Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A., Jimenez E., Varas A., Zapata A.G.; Expression and function of the Eph A receptors and their ligands ephrins A in the rat thymus."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317286; AAK00944.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin. 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
                                          181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAV 226
                                                                                                                                                                                                                                                                                                                                                                                               118 AA; 13470 MW; FF0277F079783A46 CRC64;
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.0%; Score 586; DB 11
Best Local Similarity 72.4%; Pred. No. 3e-53;
Matches 110; Conservative 3; Mismatches
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(TrEMBLrel, 19, I
                                                                                                                         PRELIMINARY;
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01-DEC-2001 (TrEMBLre
01-DEC-2001 (TrEMBLre
EPHRIN A3 (FRAGMENT).
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Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen P.B., Rodger J., Dunlop S.A., Beazley L.D.; "Ephrin homologs are expressed in the adult lizard visual system."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                        6 LLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPH
                                                    17;
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8
Query Match
32.6%; Score 424.5; DB 13; Length 202;
Best Local Similarity 45.4%; Pred. No. 3.8e-36;
Matches 84; Conservative 28; Mismatches 56; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.2%; Score 406; DB 13; Length 88; 75.0%; Pred. No. 1.1e-34; ive 7; Mismatches 9; Indels
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Last annotation update)
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Best Local Similarity 75.09
Matches 72; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                             NCBI_TaxID=7955;
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                                                                                                                                                                                                                                          Arakawa T., Hara A., Fukunishi Y., Koshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alibata A., Ashibata T., Bono H., Kasukawa T., Saito R., Kadota T., Casavant T., Saito T., Okazaki Y., Ashiburner M., Batalov S., Casavant T., Redota K., Matsuda H.A., Ashiburner M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hasebawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IQRYTPFPLGFEFLPGETYYXISVPTPESPGRCLRLQVSVCCKESGSSHESAHPV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.2%; Score 406; DB 11; Length 206; Best Local Similarity 46.9%; Pred. No. 3.3e-34; Matches 82; Conservative 19; Mismatches 62; Indels 11:
                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
10 DayS EMBRYC CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2610529M21, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675E32971D1C6EBC CRC64;
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08, Last sequence update)
19, Last annotation update)
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                206 AA.
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                                           01-JUN-2001 (TrEMBLrel. 17, Created)
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                PRT;
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MEDLINE-21085660; PubMed=11217851;
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EMBL; AK012195; BAB28092.1; -.
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PROSITE; PS01299; EPHRIN; 1.
SEQUENCE 206 AA; 22859 MW;
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InterPro; IPR001799; Ephrin.
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                PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGE---- 201
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Durbin L., Brennan C.H., Shiomi K., Cooke J.; "Eph signalling is required for segmentation and differentiation of the somites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
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01-JUN-2001 (TIEMBLIEL. 17, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
ADULT MALE TONGE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2310004J15, FULL INSERT SEQUENCE.
                                                                                                                                                                                   Submitted (UUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ006838; CAA07264.1; -. InterPro; IPR001799; EDMII. . InterPro; IPR003006; Ig_MHC. Pfam; PF00812; Ephrin; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PROCESS, EPHRIN.
PROMIS PRO1347; EPHRIN.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SECHENCE 229 AA; Z6115 MW; 8684462F67AF6F5C CRC64;
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40.0%; Pred. No. 1e-30;
iive 25; Mismatches 59;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                              Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
"Ephrin homologs are expressed in the adult lizard visual system.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; AF209776; AAF19443.1;
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
 93 AA; 11323 MW; BD561F18D34C0F28 CRC64;
                                                        108 WECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNL
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Last annotation update)
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                                                                                                                                                                                                                                                                                          Ctenophorus ornatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 48; Conserv
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SEQUENCE
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042304;
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sator K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 YTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKR 107
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                               19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsunaga T., Davis J.G., Greene M.I.;
"Cellular and subcellular compartmentalization of adult peripheral
"Cellular system by distinctive and overlapping expression of Eph
receptors and ephrins."
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131912; AAD33515.1;
Interpro; IPR001199; Ephrin.
Probom: PF00812; Ephrin; 1.
Probom: PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   120 FKEGHSYYYISKPIYHQESQCLKLKVTV-----NG-----KITHNPQAHVNPQEK
                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
BMBL; AK009144; BAB26102.1; -.
MGD; MGI:102336; Effal.
InterPro: IPR001799; Ephrin.
InterPro: IPR00180; WD40.
PRINTS; PR01347; EPHRIN.
PRINTS; PR01347; EPHRIN.
PRODOM; P000253; Ephrin. 1.
PRODOM; P000253; Ephrin. 1.
PROSITE; PS00678; WD. REPEATS.1; UNKNOWN.1.
SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;
                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                         Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         28.2%; Score 367; DB 11; 38.3%; Pred. No. 3.7e-30; tive 23; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
26.0%; Score 338; DB 11;
Best Local Similarity 58.9%; Pred. No. 1.6e-27;
Matches 63; Conservative 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 38.39
Matches 85; Conservative
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102 AA;
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                                                                       Hayashizaki Y.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Pax protein Noi protein is required for commissural axon pathway
                                                                                                                                          35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                       6
  DB 13; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formation in the rostral forebrain.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12928; CAA73391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN-A5 (FRAGMENT).
                          .4e-20;
les 22;
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20.6%; Score 268.5; ilarity 49.5%; Pred. No. 2.4e Conservative 18; Mismatches
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InterPro; IPR001799; Ephrin.
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SEQUENCE FROM N.A.
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"A systematic search for the downstream target genes of the midbrain-
MHB reciprocal inductive signaling by ordered differential display
revealed the expression of ephrin-A3 in the posterior tectum of
                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zebrafish embryös.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABB055674; BAB62805.1; -.
                                                                                                                                                                 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                     D160 PROTEIN (FRAGMENT).
                                                                                                                PRELIMINARY;
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                                                                                                                                                                 01-DEC-2001
01-DEC-2001
01-DEC-2001
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Q90231;
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Matches
                                                            RESULT 12
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitming L.,
RA Hayahizaki Y.,
RA Kanana M.,
RA Kanana M.,
RA Hayahizaki Y.,
RA Hayahizaki Y.,
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
12 DAYS EMBRYO EMBRYONIC BODY BETWEEN DIAPHRAGM REGION AND NECK CDNA,
RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:9430025D14, FULL INSERT
                                                                                                                                                                                                                                                                                                         REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQG 104
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection.";
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0
                                                                                                                                                                                              DB 13; Length 80;
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                                                                                                                                                                    1; Indels
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                                                         1
80
9674 MW; 712DDC6058214993 CRC64;
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Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    105 FKRWECNRPHAPHSPIKFSEKFQRYS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK020438; BAB32100.1; -.
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97.6%;
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
NON_TER
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 44; Conserv
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Best Local Similarity
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                                                                                                             80 AA;
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01-JUN-2001
                                                                                   NON_TER
SEQUENCE
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Q9CRL3
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                                                                                                                                        Gaps
                                                                                                                                                                                                                    9 .LLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teopterygii; Neopterygii; Cyprinidae; Cyprinidae; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLING=21290827; PubMed=11397014; MEDLING=21290827; PubMed=11397014; Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B., Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.; Morphogenesis of prechordal plate and notochord requires intact eph/ephrin b signaling."; eph/ephrin b signaling."; EMBL; AR642771; AR6427771: SEQUENCE 331 AA; 35638 MW; 6ASEACD509A09818 CRC64;
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                                                                              Length 70;
                                                                                                                          12; Indels
91F2BE4E657E10FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                              13.7%; Score 178; DB 13;
54.1%; Pred. No. 4.4e-11;
iive 14; Mismatches 12;
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70 AA; 7621 MW;
                                                                                                                                      Conservative
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Matches 70; Conserv
                                                                                                          Local Similarity
nes 33; Conserv
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DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238 1 DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTLLAS 42

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Search completed: September 28, 2002, 01:47:36 Job time: 641 sec
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SIGNAL
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MEDLING-20099673; PubMed-10633856;
Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
Wilkinson D.G., Brandli A.W.;
"Comparative analysis of embryonic gene expression defines potential
interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
Dev. Dyn. 216:361-373(1999).
EMBL, A2238666, CAB65511.1;
InterPro; IPR002086, Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                     158 QGMKVVLKVGQSPYGLPAKSPKPDSAGRINNPNPGTGNSTHPQIPP-----RGSGGENGP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 ISTPTHNL------HWKCLRMKVFVCCASTSHSGEKPVPTLPQFT-----MGPNV 190
                                                                                                                104
                                                                                                                                                                     113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 ----SRNGYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
12 ILLIFLVDLLGITAT-----NMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSD 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 KINVLEDFEGENPQVPKLEKSISGTSPKR-----EHLPL----AVGIAFFLMTF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 SSGVGPGAGPGPGGGA--EQYVLYMVSR------NGYRTCNASQGFKRWECNR
                                                                                                                                                                                                                          105 -- KPNSDMRFTIKFQEYSPNLWGHEFKTNHDYFIIAT-SDGTRQGLESMRGGVCAT----
                                                                                                                                                                                                                                                                                  173 SGEKPVPTLPQFTMGPNVK-----INVLEDFEGE--NPQVPKLEKSISGTSPKREH
                                                                                           ||| | | || || 65 P------PGPRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranjata; Vertebrata; Euteleostomi;
Mphibloi; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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12.6%; Score 164.5; DB 13; Length 327;
Best Local Similarity 26.6%; Pred. No. 8e-09;
Matches 63; Conservative 31; Mismatches 78; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4BB0FA39D4C22DCD CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN-B3 PRECURSOR.
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Probom; PP00253; Ephrin; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS01299; EPHRIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                  222 LP-----LAVGIAFFLM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 LPASNIAVIAGAAGGSAFLLL 233
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SEQUENCE 327 AA; 35913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q9PT69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                       01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAY-2001 (TrEMBLrel, 17, Last annotation update)
EPHRIN-B2 PRECURSOR.
Gallus gallus (Chicken).
Evaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Menzel P., Pasquale E.B.;

Menzel P., Pasquale E.B.;

"Coding sequence of chicken ephrin-B2.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF180729; AAD53948.1;

InterPro; IPR001799; Ephrin.

Prom: PF00812; Ephrin.

Probom: P0002533; Ephrin.

PROSITE; PS01299; EPHRIN; 1.
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333 AA.
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36761 MW;
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Best Local Similarity 27.1%
Matches 61; Conservative
PRELIMINARY;
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333 AA;
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Run on:

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AK057845 Homo sapi
Y09668 D.rerio mRN
Y09669 D.rerio mRN
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AC104327 Mus muscu
AF317286 Gallus ga
AR023765 Sequence
L40932 Gallus gall
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AC098750 Rattus no
x90377 G. domesticu
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AR080871 Sequence
AR164469 Sequence
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BC017722 Homo sapi
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AR103236 Sequence
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Beckmann, M. Patricia. and Cerretti, D. P.
Cytokines that bind the cell surface receptor Patent: US 5738044-A 3 14 *APR-1998;
Location/Qualifiers
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Pred. No. 2e-125;
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1 (bases 1 to 636)
Beckmann, M. Patricia and Cerretti, D.P.
Brotkines that bind the cell surface receptor
Patent: US 6274117-A 3 14-AUG-2001;
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Pred. No. 2e-125;
Mismatches 0;
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Sequence 3 from patent US
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Beckmann, M.Patricia. and Cerretti, D.P.
Antibodies that bind hek ligands
Patent: US 5969110-A 3 19-OCT-1999;
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Beckmann, M. Patricia. and Cerretti, D.P.
DNA encoding cytokines that bind the cell
Patent: US 5516658-A 3 14-MAY-1996;
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HSU14188 636 bp mRNA linear PRI 04-FEB-1995
Human receptor tyrosine kinase LERK-4 (EPLG4) mRNA, complete cds.
U14188 1 GI:642834
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1 (bases 1 to 536 Kozlosky, C.J., Maraskovsky, E., McGrew, J.T., VandenBos, T., Teepe, M., Kozlosky, C.J., Maraskovsky, E., McGrew, J.T., VandenBos, T., Teepe, M., Cerretti, D.P. and Beckmann, M.P.
Ligands for the receptor tyrosine kinases hek and elk: isolation of oncogene 10 (2), 299-306 (1995)
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Submitted (01-SEP-1994) Immunex Corp.,
WA 98101, USA
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/organism="Homo sapiens"
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AFPVGSPGESGTSWRGGDPPSPLCLLLLLLLLLLLRILL"
353 c 331 g 263 t
                                                                                                                  Department of Immunology, The 0310 n-Oslo, NORWAY
                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                      Aasheim, H.C.

Direct Submission
Submitted (29-MAY-1998) Aasheim H.C., Department of Immunolo Norwegian Radium Hospital, Montebello, 0310 n-0slo, NORWAY (2) (bases 1 to 1181)
Aasheim, H.C., Munthe, E., Funderud, S., Smeland, E., Beiske, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ephrin-A4"
/function="ephrin-A4 protein, membrane bound form"
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                                                                                                                                                                                   Logtenberg, T. Identification and characterization of a putative secreted variants of the ephrin-A4 (Lerk-4) ligand for Eph receptor kinases expressed in cells of the B cell lineage
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Pred. No. 1.8e-125;
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/note="leukemia"
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Mammalia; Eutheria;
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/db_xref="G1:642835"
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/note="putative"
/product="unnamed"
a 202 c 186 g
                                                                                                                    /gene="EPLG4"
/note="putative"
94. .630
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 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAG
                                                                                                                                                                   TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGTCCAGCCTCCGGCCACGTAGTCTAC
                                                                                                                                                                                                            241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC
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Eukaryota; Metazoa;
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/evidencc=experimental
/protein_id="CAMO6993.1"
/db_xref="GI:3821237"
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FGHVQFSEKIQRFTPFSLGFEFLPGETYYISVPTPESSGQCLRLQVSVCCKERNLPS
HPKRPESSQDPLEEEGSLLPALGVPIQTDKMEH"
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Aashelm, H.C., Munthe, E., Funderud, S., Smeland, E., Beiske, K. and
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ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Homo sapiens mRNA for ephrin-A4 protein, soluble form.
AJ006353
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Catarrhini; Hominidae;
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Best Local Similarity 100.0%; Pred. No. 7.1e-96;
Matches 497; Conservative 0; Mismatches 0;
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/tissue_lib="Reh cDNA library"
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Submitted (29-MAY-1998) Aasheim H.C., D
Norwegian Radium Hospital, Montebello,
                                                                                                                                                                                                                         989
                                                                                                                                                                                            CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
                                                                                                                                                                                                            /organism="Homo saplens'
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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/function="ephrin-A4
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28. 600
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/translation="MLLRLGLIYPPTRPPAPPGPLVPLLRTVLWAALLGSRLPGCSSL
RHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPHYESPGPPEGPETFALYMVDWSGYE
ACTAEGANAFQRWNCSMPFAPFSPVRFSEKIORYTPFPLGFEFLPGETYYISVPTPE
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                                                                                                                                                                                                                      Euteleostomi;
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Flenniken, A.M., Gale, N.W., Yancopoulos, G.D. and Wilkinson, D.G.
Distinct and overlapping expression patterns of ligands for
Eph-related receptor tyrosine kinases during mouse embryogenesis
Dev. Biol. 179 (2), 382-401 (1996)
                                                                                                                                                                                                                                                    Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-FEB-1997) Developmental Neurobiology, National Institute for Medical Research, The Ridgeway, London NW7 1AA,
                                                                                                                                                                                                                      Vertebrata;
אווא musculus ligand LERK-4 mRNA, complete cds.
U90663
                                                                                                                                                                                                                      Craniata;
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/product="ligand LERK-4"
/protein_id="AAB50238.1"
/db_xref="GI:1906017"
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Flenniken, A.M. and Wilkinson, D.G.
Direct Submission
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25. .699
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SPGRCLRLQVSVCCKESGSSHESAHPVGSPGESGTSGWRGGHAPSPLCLLLLLLLLPIL
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1 (basas 1 to 175826)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bordon, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burnell, K.L., Byrd, N.C., Carron, T.F.,
                                                                                                                                                                                                                       77 CGGGCCCGCTGGTTCCCCTGCGGACTGTGCTCTGGGCCGCGCTGCTCGGCTCGCGCC 136
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                                                                                                               Score 419.2; DB 10;
Pred. No. 2.7e-79;
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Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Covien, C., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Daderich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabis, A., Gavera, W., Gunaratne, P., Hanes, Garzan, V., Gill, R., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hanes, A., Jackson, L.E., Jacobson, B., Jay, Y., Johnson, R., Jolloway, C., Honsier, C., Kartison, E., Howards, O., Hodgson, R., Jolnson, R., Jolnson, R., Joudet, S., Joudah, S., Karlisson, E., Kally, S., Khan, U., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Lid, J., Liu, J., Liu, J., Liu, J., Liu, J., Ludier, R., Ludier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Mattin, R., Martingale, A., Martinez, E., Massey, E., Mawhiney, E., Mattin, R., Martinglale, A., Martin, R., Martin, M., Okwoud, G., Oragunye, N., Nickerson, E., Necken, M., Okwoud, G., Oragunye, N., Nickerson, E., Necken, M., Okwoud, G., Oragunye, N., Nickerson, E., Necken, S., Schere, S., Scotte, G., Shen, H., Shooshtari, N., Sisson, I., Sodergran, E., Sonaike, T., Sparks, A., Stanley, H., Suton, A., Store, Mall, Tamerisa, Thomas, N., Tamerisa, Thomas, S., Usmani, K., Yasquez, L., Vera, V., Villalon, D., Villaon, D., Villanson, D., Villan, C., Wul, Y., Wul, Y., Wul, Y., Wul, Y., Wul, Y., Walliamson, A., Walliams, G., Walliams
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 22 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (22-JAN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2000 this sequence version replaced gi:9719697.

Center: Baylor College of Medicine
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Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: hgsc.help@bcm.tmc.edu
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Unpublished
2 (bases 1 to 175826)
Worley, K.C.
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21031: contig of 21031 bp in length

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CE MUZDYD. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burder, M., Brown, B., Brown, M., Eryant, N.P., Buhay, C., Burch, R., Carter, M., Carazos, S.R., Chacko, J., Chen, G., Chen, G., Chen, R., Carter, M., Cavazos, S.R., Chacko, J., Cherce, D., Chen, G., Chen, R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Delaney, K.R., Daylado, D., Coyle, M.D., Dathorne, S.R., David, R.R., David, R.R., David, R.J., Daylado, C., Davy-Carroll, J.L., Defert, J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gablis, H., Gauvara, W., Gunzartne, P., Harenandez, J., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jal, Y., Johnson, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLed, M., Mortson, N., Martinez, E., Massey, E., Mawhiney, E., McLed, M., Mortson, M., Mortis, S., Massey, E., Mawhiney, E., McLed, M., Mortis, S., Massey, E., Mawhiney, E., McLed, M., Mortis, S., Massey, E., Mawhiney, E., McLed, M., Stanley, H., Peery, J., Perez, L., Peter, M., Morgan, M., Nouven, W., Nouven, M., Sodergren, E., Sodergren, E., Sodergren, E., Sodergren, E., Sodergren, E., Sodergren, S., Scott, G., Shen, H., Sutton, A., Warting, M., Tansey, J., Tansey, M., Ta
                                                                                                    ACUMB/30

85907 bp DNA linear HTG 21-DEC-2001
Rattus norvegicus clone CH230-54E23, *** SEQUENCING IN PROGRESS
***, 50 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-NoV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77039, USA on Dec 21, 2001 this sequence version replaced gi:16572779.
                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project Information
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AC098750.2 GI:17975664
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 95907)
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                                                                                                                                                                                                                                                                                                                                           Rattus.
                                                                                                                                               DEFINITION
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REFERENCE
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                                                                                                                                                                                         ACCESSION
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                                                                                  RESULT 1
AC098750
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 115410 CAGGTTGCTTCGAGGAGACGCCGTGGTGGGCCTCGACCATTACCTAGACATTGT 115469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 CTGCCCCCACTACGAAGGCCCCAGGGCCCCTGAGGGCCCCGGAGACGTTTGTTGTACAT 257
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of 10256 bp in length
unknown length
                                                                                                                                                                                                                                                                     ot 12352 bp in length
unknown length
                                                                                                  contig of 17991 bp in length
gap of unknown length
contig of 13210 bp in length
gap of unknown length
                                                                                                                                                                                         of 11230 bp in length
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                                           unknown length
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46653 c 47059 g 40343 t
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gap of unknown l
contig of 2674 b
gap of unknown l
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gap of unknown 1
contig of 1613 b
gap of unknown 1
                                                                                                                                                                                     contig of 11230
gap of unknown learners of 10256
gap of unknown learners of 12352
gap of unknown learners of 8894 b
                                                             17042
                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
of 4525
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gap of unknown
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/db_xref•"taxon:9606"
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.00448:
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75709
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186 CCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCTGAGGGCCCCGAGACGTT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 CTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC
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0; Mismatches 52

    .95907
    /organism="Rattus norvegicus"

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gap of unknown 1
contig of 1420 b
                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 1106
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80.7%; Pred. No. 4.86
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/clone="CH230-54E23"
23496 c 22932 g 221
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                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                          Consensus quality: 73847 bases at least Q40
Consensus quality: 80027 bases at least Q30
Consensus quality: 84314 bases at least Q30
Estimated insert size: 73738; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
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AC104632 289579 bp DNA linear HTG 29-DEC-2001
Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
SEDUENCE, 72 unordered pieces.
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                                                                                                                1306 CCCTTGTGCCCCACAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTA 1365
                                                                                                                                                                                                                              306 CTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG-----GCCATGTTCAATTCTCAGA 356
                                                                                                                                                                                                                                                                                             357 GAAGATTCAGGGGTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGACTTA 416
                                126 CTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTA 185
                                                                                                                                                              TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC 305
   Gaps
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                                                                                                CCTAGACATTGTCTGCCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTT
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/gene="Epl4"
join(U92889:1:<435. .547,1321. .1616,1943. .2011,2361. .3226)
/gene="Epl4"
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Mus musculus LERK-4 (Epl4) gene, exons 2, 3, 4, and complete cds.
092890
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//b_xref="G1:2843.10"
//translation="WRLIPILNT"/WAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDA
VVELGFNDYLDIFCPHYESPGPPEGPETFALYMVDWSGYFACTAEGANAFQRNNCSMP
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SSHESAHPVGSPGESGTSGWRGGHAPSPLCLLLLLLLLLLLLLLLLRLRVL"
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Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
conservation of introd-exon structure
Genomics 47 (1), 131-135 (1998)
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Sciurognathi; Muridae; Murinae; Mus.
                                            /product="LERK-4"
join(U92889.1:435. .547,1321. .1616,1943. .2011,2361.
/gene="Ep14"
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Submitted (11-MAR-1997) Molecular Biology, Immunex Corp.,
University Street, Seattle, WA 98101, USA
Location/Qualifiers
1. .3226
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Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING DRAFT
SEQUENCE, 66 unordered pieces.
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Hua,A. and Roe,B.A.
Burect Submission
Submission
Submission
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, 67 33019, USA
On Dec 24, 2001 this sequence version replaced gi:17439220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 326750)
                                                                                                                                                                                      216762 CITCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTCTCAGA 216703
                                    Db 216942 CCCTTGTGCCCAAGGTTGCTCCGAGGAGATGCCGTGGTGGGGGGTTCAACGATTA 216883
                                                                                     Db 216882 CCTAGACATCTTCTGCCCAATATGAAAGCCCAGGGCCCCCAGAAGGCCGGGAAACCTT 216823
                                                                                                                                   216822 TGCATTATACATGGTGGACTGGTCAGGCCTACGAGGCCTGCAGGGGGGAAATGC 216763
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                                                                                                                                                                        CTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG-----GCCATGTTCAATTCTCAGA 356
                                                                                                                                                                                                                        357 GAAGATTCAGGCGTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
                        CTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTA 185
                                                                       CCTAGACATTGTCTGCCCCCACTACGAAGGCCCCAGGGCCCCTGAGGGCCCCGGGAGACGTT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 981)
Menzel, P., Valencia, F., Godement, P., Dodelet, V.C. and Pasquale, E.B. Ephrin-A6, a new ligand for EphA receptors in the developing visual
                            38838 TGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGGCAAATGC 38779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 981)
Pasquale, E. B. and Menzel, P.
Pinet Submission
Submitted (27-ocr-2000) The Burnham Institute, 10901 N. Torrey
Pines Rd., La Jolla, CA 92037, USA
Location/Qualifiers
1. 981
/organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCCAAGTGTCCATCAATGACCACCTGGATATTTACTGCCCCCATTACTCGCCCCCACG 180
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/note-"ligand for EphA receptors"
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Flanagan,J.G. and Cheng,H.-J.
EPH receptor ligands, and uses related thereto
batch: US 5795734-A 3 18-AUG-1998;
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Human pancreatic c

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Human differential DNA encoding novel HEK4 binding prote Human AL-1 cDNA.
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AAV42926 AAS92024 AAT32699 AAX32767 AAT32700

AAH81578 AAS92779 AAT34292 AAT18897

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1 GCCAGACCAAACCGGACCTC.....TTCTGCGAATTCTGTGAGCC 636
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAA09469 AAK77253 AAC48024 AAS78101 AAI99683 AAQ75423

AAS75651 AAA76267

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                             The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek seningen. Hek-L also binds the elk tyrosine kinase receptors.
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100.0%; Pred. No. 4.1e-154;
iive 0; Mismatches 0;
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                        (IMMV) IMMUNEX CORP.
                                                                      WPI; 1995-106811/14.
                                                                                   P-PSDB; AAR71482
                                             Beckmann MP,
09-MAY-1994;
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Best Local Si
Matches 636;
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Human; protease; drug development; cell proliferation; placenta; kidney; cell differentiation; cell signalling; thyroid gland; leucocyte; ovary; lung; colon; prostate; eye; ds.
"Human protease #2"
                                                                                                                                                                                              Location/Qualifiers
2076..9794
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                                                                DNA; 17138
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/product= "F
2076..2154
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4105..4181
/*tag= f
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/*tag= 1
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3467..4104
/*tag= e
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/*tag= g
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5049..5052
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                                                                                                                       Human protease genomic DNA
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                                                               AAS14757 standard;
                                                                                                                                                                               Homo sapiens
                                                                                                    16-JAN-2002
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The invention relates to human protease polypeptides and polynucleotides which are expressed in the placenta, lung, ovary, colon, kidney, thyroid gland, prostate, eye and leucocyte. These sequences can be used as models for the development of human therapeutic targets, in the identification of therapeutic proteins and serve as targets for the development of drugs that modulate protease activity in cells and tissues expressing protease. The nucleic acid molecules are also useful in biological assays for detecting changes in protease nucleic acid expression and for producing proteases, which are important for regulating cell proliferation, differentiation, and signalling processes. This sequence represents genomic DNA encoding a human protease polypeptide.
                                                                                                                                                                                                                                            61 TGGCCGCGCTCCTCGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
                                                                                                                                                                                                                                                                           121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGGCGCCGTGGTGGAGCTGGGCCTCAAC 180
                                                                                                                                                                           Gaps
                                                                                                                                                                                             Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy; diagnosis; transgenic animal; ss; ds.
                                                                                                                                                     Length 17138;
                                                                                                                          Sequence 17138 BP; 2315 A; 3492 C; 3363 G; 2751 T; 5217 other;
                                                                                                                                                                          40; Indels
                                                                                                                                                      Query Match 21.1%; Score 134; DB 22; Best Local Similarity 80.5%; Pred. No. 1.4e-24; Matches 169; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                     16346 gegeteeegggetttgegegegeege 16375
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                                                                                                                                                                                                                                                                                                                                                                                     AAT15009 standard; cDNA; 783 BP
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94US-0308814
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86..688
86..688
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686..783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken elf-1 cDNA.
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19-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beasley EM;
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'number= "Intron 12"
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number= "Intron 14"
607..8911
                                                                                                                                                                          "Intron 11"
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'number= "Exon 15"
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               *tag= r
'number= "Exon 9"
                                                     "Intron
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7690..7838
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8393..8485
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8486..8606
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9713..9791
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P-PSDB; AAU08749.
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                                                                                                                                                                                                                    chicken cDNA clone (AAT15009) codes for a novel EPH receptor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 ccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacaccgt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                        Murine and chicken EPH receptor ligand, {\rm Elf}-1 - useful in diagnosis and treatment of disorders associated with the {\rm Elf}-1 gene, e.g.
                                                                                                                                                                                                                               Elf-1 (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from a day-3 chick embryo cDNA library using mouse Elf-1 cDNA (see AAT15008) as probe. The cDNA can be used for the prodn of recombinant Elf-1, in the breeding of transgenic animals, for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCCTCGGCTTTGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.6; DB 17; Length 783;
Pred. No. 9e-22;
0; Mismatches 124; Indels 6;
                                                                                                                                                                                                                                                                                                                                                            Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding an avian Elf-1 protein.
                                                                                                                                                                                     Claim 36; Page 87-88; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                        and treatment of disorders as
dementia, tachycardia , etc.
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Local Similarity 62.0%;
hes 212; Conservative (
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             (HARD ) HARVARD COLLEGE
                                          Cheng H, Flanagan JG;
                                                                          WPI; 1996-188446/19.
P-PSDB; AAR94767.
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Best Local S
Matches 212
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The present sequence encodes an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a physosine klaase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonisming intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of meuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival e.g. treatment of Alzhemmer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 CCATGTTCAATTCTCAGAGAGATTCAGGGGTTCACACCTTTCTCCCTGGGTTTGAGTT 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9e-22;
0; Mismatches 124; Indels

    for production of Elf-1 protein, useful for regulat
proliferation, differentiation, and survival of cells

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Columns 73-76; 53pp; English.
Location/Qualifiers
                                                                                                                             /*tag= b
/product= Elf-1
86..148
*tag= c
686..783
/*tag= d
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94US-0308814.
95US-0393462.
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Matches 212; Conservative
                                                                  /*tag= 86..688
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27-FEB-1995;
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CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCCTCAACGATTACCTAGACAT
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                                                                                                                                                                                                                                               480 CTGCTGC 486
                                                                                                                                                                                                                                                          lmmunogen; ss.
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30-AUG-1993;
03-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1994;
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AAQ85887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA encodes an Eph transmembrane tyrosine kinase family ligand designated Ef1-2. Ef1-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                        Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligands which bind Eph family receptors - used in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 1070;
                                                                                                                                                                          Ef1-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
neurological disorder; identification; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                          Goldfarb M, Maisonpierre PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.1%; Score 115.4; DB 16; Length Best Local Similarity 55.6%; Pred. No. 3.9e-20; Matches 271; Conservative 0; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1070 BP; 196 A; 341 C; 334 G; 189 T; 10 other;
                                       399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC
                                                                                                                                                                                                                         Location/Qualifiers
46..750
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 58pp; English.
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/product= Efl-2
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                                                                                                                                                                                                                                                                                                                                    94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
                                                                                               AAT03883 standard; DNA; 1070
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                                                                                                                                                                                                                                                                                                                                                                                       (REGE-) REGENERON PHARM INC.
                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                         Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-358635/46.
P-PSDB; AAR82605.
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                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                      21-OCT-1994;
                                                                                                                                    16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                        Aldrich TH,
Yancopoulos
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AAT03883
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288 gtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgccaggccagggctt 347
GTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC---AGAGGGCCC
                                                                                                                                                                                                                                                                                                                                                     TGTCTGCCCCCACTAC------GAAGGCCCAGGGCCCCTGAGGGCCCCGAGAC
                                                                                                                                                                                                                                      CCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCCATGTTCAATTCTCAGAGAA
                                                                                                                                                                                                                                                                                    348 caagegetgggagtgcaaceggeegeacgeecegeacageeceateaagtteteggagaa
                                                                                                                                                                                                                                                                                                                              360 GATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                   CTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ85887 standard; cDNA to mRNA; 1037 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
83..799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hek-L protein cDNA clone A2.
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93US-0114426.
93US-0161132.
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83..139
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140..796
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                                                                                                                                                                                                                                                                            75 CGGCTCCCCTCTGCGGGGGGTCCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
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                                                                                                                                                                                                                                                                                                                                                135 CCCCAGGTTGCTTCGAGGAGGCCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
                                                                                                                                                                                                                                                                                                                                                                       205 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 264
                                                                                                                                                                                                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 ---AGAGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 ccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggat 564
                                          The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek senilyen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                       15 GACCTCGGGGCGATGCGGCTGCTGCCCCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early inflammatory response; marker; antibody; therapy; induction; lipopolysaccharides; cytokines; Interleukin-2; IL-2; INF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 ggcccaagggcccggagggggcgctgggaaaccggcatgcggtgtactggaacagctccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                         231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG
                                                                                                                                                                                                          Score 103.4; DB 16; Length 1037;
                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                     Pred. No. 4.7e-17;
0; Mismatches 201; Indels
                                                                                                                                                                        Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;
 diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ24595 standard; cDNA to mRNA; 1438 BP
                      Claim 1; Page 34; 45pp; English.
                                                                                                                                                                                                         Ouery Match 16.3%;
Best Local Similarity 54.3%;
Matches 271; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 CCAGGTGTCTGTCTGCTGC 486
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Poly(A)+ mRNA isolated from human umbilical vein endothelial cells (HUVE) was treated with TNF cyclohexamide and used to construct a lambda gill cDNA library. The library was screened using radiolabelled cDNA inserts were isolated may be some of B61 BNA. Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf (+) for sequencing. Clone B61.1 contained the entire OFR encoding a protein of 205 residues (24 kb). The B61 gene is involved in early inflammatory response and serves as a marker. It may be detected by inflammatory response and serves as a marker. It may be detected by corbes or by antibody-based immunoassay of biological fluids such as plasma, CSF or urine. These assays make it possible to predict a worsening in a disease process and allow the quantitative assessment of the magnitude of the inflammatory response. This information will allow the earlier admin. Of appropriate therapy, thereby shortening the disease process and limiting the patient's exposure to anti-inflammatory/immunosuppressive therapy. B61 induction is rapid and profound, hence it is easily detectable. The B61 response is highly specific to proinflammatory stimuli, being only made by cells exposed to lipopolysaccharides or cytokines such as IL-2 and TNF and not growth factors or interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGGGGGGCTCCAGCCTCCGCCACGTAG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene prod. used as marker to detect inflammatory response detecting the B61 gene in biological fluids or by using hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.0%; Score 101.8; DB 13; Best Local Similarity 56.9%; Pred. No. 1.3e-16; Matches 253; Conservative 0; Mismatches 177;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 3; 39pp; English.
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                                                                                                                                                                                      polyA_signal
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Length 1480;

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Query Match
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CDNA encoding EBP having the N-terminal NH2-DRHTVFWN SSNPKFRNEDYTING was cloned and sequenced and, as expected, found to be identical to the B61 gene. The EBP gene expressed in CHO cells resulted in at least two polypeptides having different mol. wts. C-terminal sequencing revealed only the sequence RENAA-COOH which indicated a polypeptide of 150 amino acids (EBP1-150).
  --TGGCCATG 343
                                                   344 TICAATICICAGAGAATICAGCGCTICACACCTIICTCCCTCGGCTIIGAGTICTIAC 403
                                                             404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
                                                                                                                             438 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 497
                        321 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg
                                                                                                                                                                                                                                                                                                                                              eck receptor; eck receptor binding protein; EBP; B61; cancer; inflammation; wound; cytokine; protein tyrosine kinase; PTK; phosphorylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor binding proteins - useful for treating cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Welcher AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1480 BP; 359 A; 421 C; 393 G; 307 T; 0 other;
AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parker VP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 27-28; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
74..691
/*tag= a
                                                                                                                                                                  498 ggttgaaggtgactgtcagtggcaa 522
                                                                                                                                                      464 GGCTCCAGGTGTCTGTCTGCTAA 488
                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fox GM,
                                                                                                                                                                                                                                             AAQ63770 standard; DNA; 1480
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93US-0145616.
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P-PSDB; AAR53634.
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09-NOV-1993;
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                                                                                                                                                                                                                                                                      AAQ63770;
                                                                                                                                                                                                                                                                                                                         B61 gene.
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                                                                             201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 260
                                                                                                                                                                                                                                                                              261 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccc 320
                                                                                                                                                                                                                                                                                                                            404 CTGGAGAGACTTACTACTACTACATCTCGGTGCCCACACAGAGAGTTCTGGCCAGTGCTTGA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
                                                                                                                          116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
                                                                                                                                                       141 tettetggaacagttcaaateecaagtteeggaatgaggaetaeaceataeatgtgeage 200
                                                                                                                                                                                                                                                233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
                                                                                                                                                                                                                                                                                                            293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-----TGGCCATG 343
                                                                                                                                                                                                                                                                                                                                                                       344 TICAATICICAGAGAAGATICAGCGCTICACACCTITCICCCTCGGCTITGAGTICITAC 403
                                  Gaps
                                                                                                                                                                                     TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA sequence encoding for PRO202 polypeptide.
Score 101.8; DB 15;
Pred. No. 1.3e-16;
); Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
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                               ö
 16.0%;
56.9%;
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99WO-US30095.
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2000WO-US00277
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2000WO-US03565
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99WO-US28564
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                               Conservative
                 Similarity
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09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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11-FEB-2000;
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02-DEC-1999
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Seventeen nucleic acids encoding PRO polypeptides which are useful in
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PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate bological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TMF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of those rear utricular supporting cells or
cartilage, the proliferation of inner ear utricular supporting colls or
CT-lymphocytes, the release of a cytchine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the RPO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
c to factor VIIA. The PRO polypeptides can be used in assays to identify
monocytes (collectes in binding interactions. The polymore and any account of the province of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     æ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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0; Mismatches 177; Indels
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                                                                                                                                               2000WO-US07377.
2000WO-US07532.
2000WO-US08439.
                                                                                                                                                                                                                                                               17-MAY-2000; 2000WO-US13705.
22-WAY-2000; 2000WO-US14042.
32-UNAY-2000; 2000WO-US14941.
32-UUN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.
                                                                       2000WO-US05004
2000WO-US05601
2000WO-US04414
                                   2000WO-US04914
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ME, Goddard A,
Stewart TA, Tum
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Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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P-PSDB; AAU12315.
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                                                                   24 - FEB - 2000; 2
01 - MAR - 2000; 2
20 - MAR - 2000; 2
30 - MAR - 2000; 2
31 - MAY - 2000; 2
22 - MAY - 2000; 2
02 - JUN - 2000; 2
22-FEB-2000;
24-FEB-2000;
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Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
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Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotropic; antiantic; antianthrintlammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease;
                                                                                                                403
                                                                                                                                     463
                                                                                                                                                                                                                 277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccc 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Gerritsen ME;
Mark MR, Marsters
M, Wood WI;
                                                                         337 ag --- tecaaggaceaagteegetggeagtgeaaceggeeeagtgeeaageatggeeegg
                                    293 AGGGCCCCCGGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-----TGGCCATG
                                                                                                                344 TICAATICICAGAGAAGAITCAGCGCTICACACCTITCTCCCTCGGCTTIGAGTICTIAC
                                                                                                                                                                                               104 CIGGAGAGACTIACIACIACATCICGGIGCCCACTCCAGAGAGIICIGGCCAGIGCTIGA
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                                                                                                                                                                                                                                                                                                 464 GGCTCCAGGTGTCTGTCTGCTAA 488
                                                                                                                                                                                                                                                                                                                                                                                                              AAC90574 standard; cDNA; 1496
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2000WO-US04341.
2000WO-US04342.
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2000WO-US05841.
2000WO-US06319.
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99US-0145698.
99US-0146222.
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2000WO-US07532.
2000WO-US08439.
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Goddard A, Gouder
MF, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-025251/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO202 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound healing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB50962
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02-DEC-1999;
16-DEC-1999;
11-FEB-2000;
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18-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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21-MAR-2000;
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30-NOV-1999
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WO200073348-A2
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10-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2000;
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20-DEC-1999;
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                                                                                                                                                                         29-OCT-1999
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                                        07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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                                                                                                         22-JUN-
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Matches
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                                                             The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a manmal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosolarosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or anglogenic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343
                                                                                                                                                                                                                                                                                                                                    56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGGGGGGCTCCAGCCTCCGCCACGTAG 115
                                                                                                                                                                                                                                                                                                                                                           97 tectetggggecetetettgggtetgtgetgeagtetggeegetgetgategeeacaceg 156
                                                                                                                                                                                                                                                                                                                                                                                       116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGGCGCCGTGGTGGAGCTGGGCC 175
                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccc 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 agaagetgtetgaagagttecagegetteacacettteaceetgggeaaggagtteaaag 453
                                                                                                                                                                                                                                                                                                            Gaps
diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG - - - CCCAGGGCCCCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-----TGGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 TICAATICTCAGAGAAAAAITCAGCGCTICACACCTTICICCCTCGGCTTTGAGTTCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                  157 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc
                                                                                                                                                                                                                                                                               16.0%; Score 101.8; DB 22; Length 1496; 56.9%; Pred. No. 1.3e-16;
                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                         Sequence 1496 BP; 362 A; 427 C; 398 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                         0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 GGCTCCAGGTGTCTGTCTGCTAA 488
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                                                                                                                                                                                                                                                                                              Best Local Similarity 56.9
Matches 253; Conservative
             disorders in a mammal
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO202 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001
                                      Claim 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC91576;
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233
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The present sequence is one of twenty eight nucleic acids encoding PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, atrooptal, hypothalamic and other glandlar, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGGGGGCTCCAGCCTCCGCCAGGTAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 tectetgggecectetettgggtetgtgetgeagtetggeegetgetgategeeacaceg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 tettetggaacagtteaaateecaagtteeggaatgaggaetaeaceatacatgtgeage 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kabakoff RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are useful
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other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1496 BP; 362 A; 427 C; 398 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Twenty eight nucleic acids encoding PRO polypeptides for treating various tumors, e.g. breast cancer, and inflammatory, anglogenic and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hebert C,
Wood WI;
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Fig 47; 188pp; English.
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2000WO-US03565
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2000WO-US06319
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99WO-US20111
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2000WO-US14941
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Smith V,
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11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
  30-MAY-2000;
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31-JAN-2001; 2001WO-EP01003
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                                                                                         337 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 393
                                                                                                                       403
                                                                                                                                   463
                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antlinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                    277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccc 336
                                                                  343
                                                                                                                                                                                                      513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
            GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG
                                                                                                                                                                                                   454 aaggacacagetactactacatetecaaacecatecaceageatgaagacegetgettga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                               293 AGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-----TGGCCATG
                                                                                                                     344 TICAATICTCAGAGAAGATICAGCGCTICACACCTITCTCCCCTCGGCTITGAGTICTIAC
                                                                                                                                                                        404 CTGGAGAGCTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                           Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 531-532; 1379pp; English.
                                                                                                                                                                                                                                 GGCTCCAGGTGTCTGTCTGCTGCAA 488
                                                                                                                                                                                                                                                           ggttgaaggtgactgtcagtggcaa 538
                                                                                                                                                                                                                                                                                                                            AAC98823 standard; cDNA; 1527 BP
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P-PSDB; AAB54058.
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                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001
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detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and tharget the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to creat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 tettetggaacagtteaaateecaagtteeggaatgaaggaetacaeecatacatgtgeage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101.8; DB 21; Length 1527;
Pred. No. 1.3e-16;
0; Mismatches 177; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                             sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human differential transcription-associated cDNA SEQ ID 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1527 BP; 397 A; 426 C; 394 G; 308 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || | |||||| ||||| | ||||| ggttgaaggtgactgtcagtggcaa 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
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Best Local Similarity 56.9%;
Matches 253; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                     between tumour accitions a mucrate and vice that separate activity. (1)

work as modulators of Ras activity by inducing expression of tumour

suppressor genes. (1), and polypeptides encoded by them, are useful as

targets for diagnosis or therapy and in screening to determine the

effects of an active compound (potential pharmaceutical) on a cell line,

particularly for diagnosis and treatment of tumors, especially by

modulating expression of (1) (by gene therapy, antisense RNA or ribozyme

polypeptides (by administration of the polypeptide or its activator,

antibody (optionally as a conjugate) or inhibitor). The method allows

identification of many class II tumour suppressor genes (i.e. genes that

are not primary targets for tumour-initiating mutations).

AAH81492-AAH82376 represent the human and rat derived nucleic acid

fragments described in the method of the invention.
                                                                                                                                                                                                                                                                                                       This invention describes a nucleic acid (I) with differential expression
                                                                                                                                                                                       Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 CCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 GGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT-----TGGCCATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 CAATTCTCAGAGAAGATTCAGCGCTTCACACTTTCTCCCTCGGCTTTGAGTTCTTACCT
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                                                                                             Tchernitsa 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.3%; Score 97.2; DB 22; Length 439; llarity 56.3%; Pred. No. 1.5e-15; Conservative 0; Mismatches 178; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 439 BP; 106 A; 130 C; 113 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Schaefer R, Zuber J,
Schmitz A, Sers C;
                                                                                                                                                                                                                                                                 Disclosure; Page 354-355; 579pp; German.
                                                     (META-) METAGEN GES GENOMFORSCHUNG MBH.
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                 31-JAN-2000; 2000DE-1004102.
                                                                                   Rosenthal A, Hinzmann b
Grios M, Hellriegel M,
                                                                                                                                                 WPI; 2001-483415/52
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nes 249; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AsS64197-As894564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                      ONA encoding novel human diagnostic protein #28583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 28583; 103pp; English.
AAS92779 standard; cDNA; 1574 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
                                                                                                                                                            (first entry)
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Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABG28592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                              AAS92779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A cDNA clone (AAT34292) codes for human HEK4 binding protein (HEK4 BP) (AAW00035), a protein that binds to and activates HEK4 and ECK
                           449
                                               242
                                                                509
          182
                                                                                     296
                                                                                                        569
                                                                                                                           356
                                                                                                                                              629
                                                                                                                                                                 GAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
                                                                                                                                                                                    689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to treat cancer and nervous system disorders
                                                        GAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGA
                           gaacagcagcaaccccagattccagaggggtgactaccatattgatgtctgtatcaatga
                                             TTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCCGAGAC
                                                                                    243 GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCA-----GGCAGAGGG
                                                                                                       ctatgtcctctacatggtgaactttgatggctacagtgcctgcgaccacacttccaaagg
                                                                                                                          297 CCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGA
                                                                                                                                             gttcaagagatgggaatgtaaccggcctcactctccaaatggaccgctgaagttctctga
                                                                                                                                                                           Ligand for EPH-like receptors, partic. the HEK4 receptor - useful modulate growth and differentiation of, e.g. liver and kidney cell
                                                                                                                                                                                                                                                                                                                                                  HEK4 binding protein; HEK4 receptor; EPH-like receptor; protein tyrosine kinase; ligand; growth; differentiation; cancer; nervous system disorder; therapy; ss.
                                                                                                                                                                                                     CTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCT 460
                                                                                                                                                                                                               Claim 15; Page 38-39; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
175..861
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                                                                                                                                                                                                                                                                       AAT34292 standard; cDNA; 1728
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                                                                                                                                                                                                                                                                                                                               HEK4 binding protein cDNA
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175..231
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232..858
/*tag= c
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P-PSDB; AAW00035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fox GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                 HEK4 binding
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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receptors. It was isolated from a human placenta cDNA library using primers (see also AATA1295-96) based on isolated peptides (AAM000365-38) of HEK4 BP. The cDNA can be used for recombinant prodn. of HEK4 BP, useful for modulating the growth and/or differentiation of EPH subfamily receptor-bearing cells. It can also be used to detect or quantitate HEK4 BP nucleic acids, to detect abnormalities in the HEK4 BP gene, or to control expression levels of HEK4 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGA
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9
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                                                                                                                                                                                                                Sequence 1728 BP; 402 A; 495 C; 401 G; 430 T; 0 other;
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                                                                                                                                                                                                                                                                                          14.9%; Score 94.8; DB 17;
51.9%; Pred. No. 8.8e-15;
iive 0; Mismatches 217;
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                                                                                                                                                                                                                                                                                             Query Match 14.9°
Best Local Similarity 51.9°
Matches 241; Conservative
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(206) 233-0644
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
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STREET: 51 UNIVERSI
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                           September 27, 2002, 22:42:54; Search time 65.52 Seconds (without alignments) 2384.355 Million cell updates/sec
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                                                                                                                                                                                                                                              US-09-904-954-3
636
1 GCCAGACCAAACCGGACCTC.....TTCTGCGAATTCTGTGAGCC 636
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                   4.5
Compugen Ltd
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US-09-920-048-3
US-08-455-001-3
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US-08-445-065-11
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-08-379-802-1
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                     GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
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Maximum DB :
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Patent No. 551668
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
PCT-US95-11869-1
PCT-US95-15781-4
US-09-609-324A-9
US-08-920-440B-9
US-09-173-492-9
US-09-173-133-9
US-09-173-133-9
US-09-173-133-1
US-09-173-133-1
US-09-173-133-1
US-09-173-131-1
US-09-15-533-1
PCT-US95-15-779-1
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US-08-920-440B-7
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US-09-173-133-7
US-09-165-533-7
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CLASSIFICATION NAMBER: US/US/240,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
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61 TGGGCGCGTTCCTCGGCTCCCCTTGCGGGGGCTCCAGCCTCCGCCAGGTAGTCTAC 120
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
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Best Local Similarity 100.0%; Pred. No. 2.2e-162;
Matches 636; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-A0C-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-A0C-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MX-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
                                               ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: MASHINGTON
     RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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28..93
                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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     TITLE OF INVENTION:
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HYPOTHETICAL: N
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LOCATION:
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; LOCATION:
US-08-453-943-3
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; Sequence 3, Application US/08453943
; Patent No. 5738844
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERETII, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
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94..630
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28..93
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28..633
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L C6
                                                                                  NAME/KEY: 1
LOCATION: 9
FEATURE:
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LOCATION:
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; LOCATION:
US-08-240-124-3
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121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGTGGAGCTGGGCCTCAAC 180
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                                                                                                            ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC
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US-09-057-121-3
Sequence 3, Application US/09057121
Factor No. 5969110
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BIN
TITLE OF INVENTION: CYTOKINE THAT BIN
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPARION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IUMBER: US 08/109,745
20-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/161,132 FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
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181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGGCCCCTGAGGGCCCCGGAG 240
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Pred. No. 2.2e-162;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 636; Conservative 0;
               REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
                                                                  TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756922
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 635 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32
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28..633
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CLONE: hek-L C6
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LOCATION:
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NAME/KEY:
LOCATION:
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US-09-057-121-3
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Length 636;

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Query Match
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 541 ACATCAGGGTGGCGAGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MANUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                 601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
                                                   601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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PRIOR APPLICATION DATA:
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 537-0430
TELERA: 756825
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/240,124
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5.09-358-734-3
Sequence 3, Application US/09358734
Patent No. 6274117
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
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LOCATION: 94..630
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28..93
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COMPUTER READABLE FORM:
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LOCATION:
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; LOCATION:
US-09-358-734-3
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FEATURE:
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GENERAL INFORMATION:
APPLICANT MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01177
CURRENT APPLICATION NUMBER: US/09/813,819
CURRENT FILING DATE: 2001-03-22
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181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCTGAGGGCCCCGAG
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100.0%; Score 636; DB 4; I
ilarity 100.0%; Pred. No. 2.2e-162;
Conservative 0; Mismatches 0;
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Patent No. 6294368
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; LOCATION: (1)...(17138)
; OTHER INFORMATION: n = A.T.C or
US-09-813-819-3
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                  Best_Local Similarity
Matches 636; Conserv
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132 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTGACGAGGAGCGCGCTGCC 291
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                                    APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 124; Indels
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Pred. No. 7.2e-24;
                                                                                                                                                                                                                                                                                        COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY/AGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%;
62.0%;
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             783 base pairs
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86..148
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                                                                                                                                                                                                                      Boston
Patent No. 5795734
                                                                                                                                                                                                                                                                                 ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
COCATION:
US-08-455-001-3
                                                                                                                                                                          ADDRESSEE:
STREET: 6
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                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT MERKULOV, Gennady et al
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOO1177DIV
CURRENT APPLICATION NUMBER: US/09/920,048
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/813,819
PRIOR FILING DATE: 2001-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 16227 tgggccgcg-tcctcggctcccttgcgcgggggttccagcctccgccacgtagtctac 16285
                                                                                                                                                                                                                                                                                                        16286 tggaactccagtaaccccaggtagccgggccgaaccgggcgaggcgacagccaagtctgc 16345
                                                                                                                                            Db 16167 gccagaccaaaccggacctcggggggggggtgctgctgctgccctgctgcggactgtccta 16226
                                                                                                                                                                                                                                      16227 tgggccgcg-tcctcggctcccctctgcgcggggggctccagcctccgccacgtagtctac 16285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
                                                                                                                                                                                                                                                                                 121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGGACGCCGTGGTGGAGCTGGGCCTCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCAGACCAAACCGGACCTCGGGGGGGGTGCGGCTGCTGCCGCTGCTGCGGGACTGTCCTC 60
                                                                                                       1 GCCAGACCAAACCGGACCTCGGGGGGGGGTGCGGCTGCTGCCCGTGCGGGACTGTCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 134; DB 4; Length 17138; llarity 80.5%; Pred. No. 8.9e-27; Conservative 0; Mismatches 40; Indels 1
                  Length 17138;
                                                              40; Indels
                    Score 134; DB 4;
Pred. No. 8.9e-27;
0; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16346 gcgctcccgggctttgcgcgccgccac 16375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GATTACCTAGACATTGTCTGCCCCCACTAC 210
                                                                                                                                                                                                                                                                                                                                                                         181 GATTACCTAGACATTGTCTGCCCCCACTAC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(17138)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09920048
Patent No. 6344352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/08455001
                  Query Match 21.1%;
Best Local Similarity 80.5%;
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
LENGTH: 17138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-920-048-3
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412 ACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTTCACCCCCTTCTTTGGGCTTCGAGTT 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 CCCCAGGTTGCTTCGAGGAGGCGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TGTCTGCCCCCACTAC-----GAAGGCCCAGGGCCCCTGAGGCCCCGAGAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC---AGAGGGCCC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GACCTCGGGGGGGGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
  339 CCATGTTCAATTCTCAGAGAATTCAGCGCTTCACACCTTTCTCCCCTCGGCTTTGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1070;
                                                                                                                                                                                                                                     Sequence 8, Application US/08299567

Patent No. 5747033

GENERAL INFORMATION:

TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL

TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE Regeneron Pharmaceuticals, Inc.

STREET: 777 01d Saw Mill River Road

CITY: Tarrytown

STATE: New York

COUNTRY: U.S.A.

21P: 10591-6707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FLADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: REPRENCE/DOCKET WUMBER: 32,143
REFERENCE/DOCKET WUMBER: 32,143
REFERENCE/DOCKET WUMBER: 32,143
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: 914-345-7721
                                                                                                               472 CGGTCCCGGCCACGAGTATACTACATCTCTGCGTCTCCCCC 513
                                                                                        399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                       US-08-299-567-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 -----CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 CGACCACCGGCAGAAGGGCTTCAAACGTTGGGAGTGCAACCGGCCCGACTCCCCCAGCGG 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
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                                                                                                                                                                                                                                                                    EPH Receptor Ligands, and Uses Related
Thereto
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Pred. No. 7.2e-24;
0; Mismatches 124; Indels
                                                               399 CITACCTGGAGACTTACTACTACATCTCGGTGCCCACTCC 440
                                                                                        472 CGGTCCCGGCCACGAGTATACTACATCTCTGCGTCTCCCCCC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/COCKET NUMBER: HMI-011CPPC
TELECOMUNICATION INFORMATION:
TELECHNOE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9511869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         APPLICANT:
TITLE OF INVENTION: EPH Receptor
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTABLE
COMPOTER: OF SYSTEM: PC-DOS/MS-DC
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Best Local Similarity 62.0%;
Matches 212; Conservative
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86..685
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MOLECULE TYPE:
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LOCATION:
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LOCATION:
FEATURE:
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; LOCATION:
PCT-US95-11869-3
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                                                                                                                                                                            OLT 8-0895-11869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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E: IMMUNEX CORPORATION 51 UNIVERSITY STREET
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                                                                                                                                                                                                   Query Match
Best Local Similarity 54.3%;
Matches 271; Conservative
                                                                                                                  mat_peptide
140..796
                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX C
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MEDIUM TYPE: Floppy
                                 83..799
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CITY: SEATTLE
STATE: WASHINGT
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LOCATION:
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LOCATION:
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US-08-240-124-1
                                                                                                                    NAME/KEY:
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   FEATURE:
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                                 300 CCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAAA 359
                                                                                                  GATTCAGCGCTTCACACCTTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGTTTTACTA 419
                                                                                                                                                                   CTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGT 479
                                                                                                                                                                                       288 GTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGGCCAT 347
                                                                                                                    348 caagcecregeagrecaaccegececacecececacaccecarcaagrecregagaa 407
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08240124
Patent No. 551658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REPERBNEMCAFOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1037 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N<sub>O</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: SEATTLE STATE: WASTE
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                                                                                                                                                                                                                                   480 CTGCTGC 486
                                                                                                                                                                                                                                                          1111111
528 CTGCTGC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98101
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                                                                                                                                                                                                                                                                                                                                     JS-08-240-124-1
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205 CCAGCACCTGGGGGGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
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                                                                                                                               75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
                                                                                                                                                                                                                                135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
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                                                    Gaps
                                                                                                15 GACCTCGGGGGGGATGCGGCTGCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
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  Length 1037;
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Patent No. 5738844
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETIT, DOUGLAS P.
APPLICANT: CERRETIT, DOUGLAS P.
ATTLE OF INVENTION: CETYOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
                                                    Indels
Score 103.4; DB 1;
Pred. No. 6.2e-19;
0; Mismatches 201;
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385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
                                                                       348 ATTCTCAGAGAAGATTCAGGGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
                                                                                                                                                                  408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
                                                                                                                                                                                            445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCGG
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US-09-057-121-1
Sequence 1, Application US/09057121
Fatent No. 5960110
Fatent No. 5960110
FAPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/161,132
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APPLICATION NUMBER: US/09/057,121
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REPERENCE/DOCKET NUMBER: 2814-C
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILLING DATE:
APPLICATION NUMBER: US 08/161,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                            468 CCAGGTGTCTGTCTGCTGC 486
                                                                                                                                                                                                                                                                                    565 GAAGGTGTTCGTCTGCTGC 583
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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IMMEDIATE SOURCE:
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ANTI-SENSE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 GGCCCAAGGGCCCGGAGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 Tracrecededracadedecedeseses 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 ---AGAGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCCATGTTCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 201; Indels
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                PRICR APPLICATION 379.

APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A,
REGISTRATION NUMBER: 32,172
RECESCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAS: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1037 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 TGTCTGCCCCCACTACGAAGGC
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Matches 271; Conservative
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140..796
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83..139
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IMMEDIATE SOURCE:
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FEATURE:
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; LOCATION:
US-08-453-943-1
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FEATURE:
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FEATURE:
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Version 5.1a

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Microsoft Word for Apple,
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140..796
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83..139
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STRANDEDNESS: single
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
IMMEDIATE SOURCE:
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LOCATION:
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LOCATION:
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; LOCATION:
US-09-358-734-1
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                                                                                                                                                                                                                                                                                                                                                              135 CCCCAGGTTGCTTCGAGGAGGCGCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                          Length 1037;
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                                                                                                                                                                                                       Indels
                                                                                                                                                                      Score 103.4; DB 2;
Pred. No. 6.2e-19;
0; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                             TGTCTGCCCCCACTACGAAGGC------
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BI.
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09358734 Patent No. 6274117 GENERAL INFORMATION:
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                                                                                                                                                                      Query Match 16.3%;
Best Local Similarity 54.3%;
Matches 271; Conservative
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83..139
                                                                                          mat_peptide
140..796
           83..799
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CITY: SEATTLE
STATE: WASHINGTON
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LOCATION:
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LOCATION:
                                                                                          ; NAME/KEY:
; LOCATION:
US-09-057-121-1
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                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 ---AGAGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
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Pred. No. 6.2e-19;
0; Mismatches 201;
                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 TGTCTGCCCCACTACGAAGGC-----
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ER: 2814-C
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
                                                                                                                                                                                                                                                                                                                         ATTOKNEIZANGENA KATHRYN ANDRE: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REPRENCE/DOCKET NUMBER: 2814
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEFAX: 756822
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base_pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.3%;
Best Local Similarity 54.3%;
Matches 271; Conservative
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116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
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                                                            321 AG---TCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCCAGTGCCAAGCATGGCCCGG
                                                                                                                                                                                    404 CTGGAGAGACTTACTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA
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Pred. No. 1.9e-18;
0; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,779
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08452779
Patent No. 5716934
GENERAL INFORMATION:
APPLICANT: Bartley, Timothy Dudley
APPLICANT: Fox, Gary Michael
APPLICANT: Boyle, William James
APPLICANT: Welcher, Andrew Avery
APPLICANT: Parker, Vann Phillips
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,616
                                                                                                                                                                                                                                                                   464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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STRANDEDNESS: double-stranded
TOPOLOGY: linear
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56.9%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1480 nucleotides
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OPERATING SYSTEM: Macintos
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Best Local Similarity 56.9
Matches 253; Conservative
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0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MD
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bartley, Timothy Dudley
APPLICANT: Fox, Gary Michael
APPLICANT: Boyle, William James
APPLICANT: Welcher, Andrew Avery
APPLICANT: Parker, Vann Phillips
TITLE OF INVENTION: Eck Receptor Ligands
WUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/145,616
FILING DATE: 09-NOV-1993
INFORMATION FOR SEQ ID NO: 11:
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STREET: Amgen Center
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08448736
Patent No. 5650504
GENERAL INFORMATION:
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TYPE: nucleic acid
                                                                                                                                                              468 CCAGGIGTCTGTCTGCTGC 486
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56.9%;
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Best Local Similarity 56.9
Matches 253; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Thousand Oaks
STATE: California
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463	4 CIGGAGAGACTTACTACTACATCTCGGIGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA	40	oy Op
403	344 TICAATICTCAGAGAAGAITCAGCGCTTCACACCTITCCCCTCGGCTTTGAGTTCTTAC 403 378 AGAAGCTGTCTGAGAGATTCCAGCGCTTCACACTTTCACCCTGGGCAAGGAGTTCAAAG 437	34	Qy Db
343	293 AGGGCCCCGGGCCTACAAGCGCTGGGTGCTCCTTGCCTTTGGCCATG 343 1	32	QY Db
320	233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTĀTGAGTCCTGCCAGGCAG 292 10	23	Qy Db
260	201 TGAATGACTACGTGGACATCATCTGTCCGCACTATGAAGATCACTCTGTGGCAGACGCTG 260	20	වූ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptodata/2/pna/US089_COMB.seq:
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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ptodata/2/pna/US080_COMB.seq:*
ptodata/2/pna/US081_COMB.seq:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pending_Patents_NA_Main:*
    /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq
    /cgn2_6/ptodata/2/pna/US06_COMB.seq:
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                                                                                                                                                                                                                                                                                                                                            21979536 seqs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptodata/2/pna/US096C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /2/pna/US6035 com.

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Result	Score	Query	Length	DB	ID	Description
	989	100.0	989	-	PCT-US94-09282-3	Sequence 3, Appli
7	636	100.0	m	2	US-08-161-132-3	m
3	636		636	Н	-09-440	e 8
4	636		636	m	-09-904	3, Ap
S	634.4	99.7	1247	25	US-09-652-122-4283	428
9	34		1247	7	-09-698-010-11	11684,
7	634.4	99.7	1247	7	-000-001-60-	
æ	21		1273	ϵ	-09-160	311, A
6	469.4		531	٦	-00-306-609-1	
10	469.4	73.8	531	٦	-09-522-251-7	7629,
11	469.4		531	3	-10-025-600-7	
12	469.4	73.8	532	7	-09-205-070-27	27545,
13	469.4		532	۲	-09-340-623-27	27545,
14	469.4	73.8	532	3	09-898-888-27	
15	469.4	73.8	532	3	US-09-898-888A-27545	27545,
16	421.8		731	7	60-360-207-78	
17	409.8	64.4	476	Н	-09-277-227-17	17412,
18	409.8	64.4	476	ϵ	09-909-627-1741	17412,
19	407.4	64.1	490	щ	-09-240-371-65	9
20	407.4	64.1	490	Ч	09-277-227-174	17411,
21	407.4	64.1	490	17	-956-163	16311,
22	407.4	64.1		ĸ	09-904-703-163	163
23	407.4			3	39-909-627-17	17411,
24	407.4	64.1		'n	09-919-724-655	Seguence 6555, Ap
25	386.4	60.8		18	US-09-465-877-15527	15527,
56	386.4			m	US-09-906-555-15527	15527,
27	361.4		39		9-	59441,
28	61		39		-09-933-524	59441,
59	361.4	56.8		35	-933-524A-59	
30	360.4		47	16	-09-240-371-7127	7127, A
31	360.4	56.7	475	16	US-09-277-227-21899	Sequence 21899, A

/cgn2_6/ptodata/2/pna/US6002_COMB.seq /cgn2_6/ptodata/2/pna/US6003_COMB.seq /cgn2_6/ptodata/2/pna/US6004_COMB.seq

'pna/US100_COMB.seq:

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Indels

Length 636;

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301 CGGGCCTACAAGCGCTGGGTGTGCTCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08161132
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SOUGHCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
                                                                                                                                                                                                            100.0%; Score 636; DB 1; I
100.0%; Pred. No. 2.2e-145;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 636; Conservative
   mat_peptide
94..630
                                                                                                                   sig_peptide
28..93
                                                                            28..633
                                                          CDS
                   LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
     NAME/KEY:
                                                                                                                 , NAME/KEY:
, LOCATION:
PCT-US94-09282-3
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US-08-161-132-3
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
CONTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION NUMBER: PCT/US94/09282
FILING DATE:
FILING 
               US-09-919-724-7127
US-09-65-122-3419
US-09-65-124-7858
US-09-65-124-1572
US-09-234-611-16562
US-09-235-768-20569
US-09-332-782-20569
US-09-737-223-20569
US-09-333-397-21074
US-09-339-397-21074
                                                                                                                                                                                                                                                     US-60-212-656-600
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
LYPE: nucleic acid
STRANDENESS: sindle
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IMMEDIATE SOURCE:
   STRANDEDNESS:
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PCT-US94-09282-3
 CLONE:
FEATURE:
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61 TGGGCCGCGTTCCTCGCCTCCCCTCTGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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                    CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG
                                                                  ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC
                                                                                                                                                                                                 TGCTGCAAGGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC
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                                                                                                                                                                                                                                                                                                                                                 CTICIGATICITCGICITCIGCGAATICIGIGAGCC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Marvey E.
TITLE OF INVENTION: Human Neurobiology Array
FLE REFERENCE: CLON-006GLTP11
CURRENT APPLICATION NUMBER: US/09/440,302A
CURRENT APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 839, Application US/09440302A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-440-302A-839
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LENGTH: 636
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100.0%; Pred. No. 2.2e-145;
ive 0; Mismatches 0;
                                                                                                               Patentin Release #1.0, Version #1.25
                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,132
                                                                                                                                                                                                                                                                                                             NAME: SEESE, KATHRYN A.
RECISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 636; Conservative
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                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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WASHINGTON
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LOCATION:
FEATURE:
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; LOCATION:
US-08-161-132-3
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                                                                                                                                                                     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCTCTGTCTTTGTTACTGCTG
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09904954
GENERAL INFORMATION:
APPLICANT: BECKENN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintols
OPENATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-01-2001
                                                                                                                                                                                                                       601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
                                                                                                                                                                                                                                     OR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE: «UDKNOWN)
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-406-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-40G-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANNI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: WASHINGTON COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
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GENERAL INFORMATION:
APPLICANT: Shyjan, andrew W.
TITLE OF INVENTION: THEREFOR
FILLE REFREENCE: 1600.1194-001
CURRENT APPLICATION NUMBER: US/09/652,122
CURRENT FLING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,421
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                                                                                                                                                                                        ; Score 636; DB 34;
; Pred. No. 2.2e-145;
0; Mismatches 0;
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                                                                                                               LOCATION: 28..93
SEQUENCE DESCRIPTION: SEQ ID NO:
mat_peptide
94..630
                                                                                              sig_peptide
                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 636; Conservative 0
                                                            28..633
                                                            LOCATION:
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NAME/KEY:
               LOCATION:
                                             NAME/KEY:
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                              FEATURE:
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FastSEQ for Windows Version 4.0

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SOFTWARE: Fast:
SEQ ID NO 11684
LENGTH: 1247
                               TYPE: DNA
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                                                                                                    Length 1247;
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GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: THEREFOR
FILE REFRENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
                                                                                                                           Indels
                                                                                                     Score 634.4; DB 25;
Pred. No. 6.3e-145;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 5020
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4283
LENGTH: 1247
                                                                                                     99.78;
                                                                                                                Local Similarity 99.8 es 635; Conservative
                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-122-4283
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Best Local Si
Matches 635;
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                                                                          ; DB 27;
.3e-145;
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECU
FITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2022-001
CURRENT APPLICATION NUMBER: US/09/700,000
CURRENT APPLICATION NUMBER: 60/162,619
PRIOR APPLICATION NUMBER: 60/162,619
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 7171
SCOFTWARE: FastSEQ for Windows Version 4.0
                                                                            Score 634.4;
Pred. No. 6.36
0; Mismatches
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                                                                          99.7%;
ilarity 99.8%;
Conservative
  sapiens
                                                                                                Similarity
                US-09-698-010-11684
ORGANISM: HOMO
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                                                                            Query Match
Best Local Simi
Matches 635;
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                                                             Score 634.4; DB 28;
Pred. No. 6.3e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PUZIJ.
CURRENT APPLICATION NUMBER: US/09/760,443
CURRENT FILING DATE: 2001-01-16
                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 311, Application US/09760443; GENERAL INFORMATION:
                                                           99.78;
                                                                                 Conservative
                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                            Ouery Match
Best Local Similarity
Matches 635; Conserv
         ; TYPE: DNA
; ORGANISM: HOMO
US-09-700-000-4952
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LENGTH: 1273
LENGTH: 1247
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM A CDNA LIBRARY OF FETAL LIVER-SPLEEN
TITLE OF INVENTION: FROM A CDNA LIBRARY OF FETAL LIVER-SPLEEN
CURRENT APPLICATION NUMBER: US/09/306,609
CORRENT RILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/168,296
EARLIER FILING DATE: 1998-10-07
EARLIER PLING DATE: 1998-10-07
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Pred. No. 1.1e-141;
3; Mismatches 1;
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99.28;
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Best Local Similarity 99.2
Matches 631; Conservative
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LOCATION: (782)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (793)
OTHER INFORMATION: n
                                                                                     NAME/KEY: SITE
LOCATION: (1069)
OTHER INFORMATION:
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Best Local Si
Matches 481
                                                                                  TYPE: DNA
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                                                                                                                                                                DB 17; Length 531;
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LIVER-SPLEEN
                                                                                                                                                                                        Indels
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Mark C.
APPLICANT: Joleson, Mark C.
APPLICANT: Garcia, Veronica E.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM A CDNA LIBRARY OF FETAL LIV
FILE REFERENCE: 718CTP
CURRENT APPLICATION NUMBER: US/09/522,251
CURRENT FILING DATE: 2000-03-09
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-05-07
EARLIER PPLICATION NUMBER: 09/306,609
EARLIER APPLICATION NUMBER: 09/168,296
                                                                                                                                                               73.8%; Score 469.4; DB 17
99.2%; Pred. No. 1.4e-104;
tive 0; Mismatches 3;
        NUMBER OF SEQ ID NOS: 13025
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7629
LENGTH: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7629, Application US/09522251
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
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                                                                                                                    or
EARLIER FILING DATE: 1997-10-09
                                                                                                                 - A,T,C
                                                                                                                                                                           Best Local Similarity 99.2
Matches 481; Conservative
                                                                             FEATURE: NAME/KEY: misc_feature
                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                    ; COCATION: (1)...(531); OTHER INFORMATION: n
US-09-306-609-7629
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM A CDNA LIBRARY OF FETAL LIVER-SPLEEN

FILE REFERENCE: 20411-718CON2

CURRENT APPLICATION NUMBER: US/10/025,600

CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-07

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-07

PRIOR PPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/168

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-07

PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-09
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Pred. No. 1.4
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 60/150,686
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 13025
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7629
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...(THER INFORMATION: n = A,T,C

US-09-522-251-7629
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ilarity 99.2%;
Conservative
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us-09-904-954-3.rnpm

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72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
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                                                           Length 532;
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                                                                                          Indels
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TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/340, 623
CURRENT FILING DATE: 1999-06-28
EARLIER APPLICATION NUMBER: US 09/205,070
EARLIER PPLICATION NUMBER: US 09/205,070
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASTERQ for Windows Version 3.0
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                                                              DB 16;
                                                            Score 469.4; DB 16
Pred. No. 1.4e-104;
0; Mismatches 3;
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                                                         73.8%;
99.2%;
 ; OTHER INFORMATION: n = A,T,C
US-09-205-070-27545
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Best Local Similarity 99.2
Matches 481; Conservative
                                                                                       Matches 481; Conservative
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COCATION: (1)...(532)
COTHER INFORMATION: n = US-09-340-623-27545
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ORGANISM: Homo sapiens
                                                            Query Match
Best Local Similarity
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US-09-340-623-27545
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LENGTH: 532
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748
CURRENT APPLICATION UNDRER: US/09/205,070
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                              73.8%; Score 469.4; DB 37; 99.2%; Pred. No. 1.4e-104; Live 0; Mismatches 3; :
NUMBER OF SEQ ID NOS: 13025
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7229
LENGTH: 531
                                                                                                                     ; LOCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or
US-10-025-600-7629
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Matches 481; Conservative
                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                       NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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LOCATION: (1)...(532)
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llarity 99.2%; Pred. No. 1.4e-104;
Conservative 0; Mismatches 3;
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Sequence 27545, Application US/0989888A

Sequence 27545, Application US/0989888A

GENERAL INFORMATION:
TITLE OF INVENTION: LIBRARIES

FILE REPERENCE: 20411-748C0N1

CURRENT APPLICATION NUMBER: US/09/898,888A

CURRENT FILING DATE: 2001-07-30

PRIOR PILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-16-20
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SOFTWARE: FastSEQ for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C
US-09-898-888A-27545
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TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FRO
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 2011-748CONI
CURRENT APPLICATION NUMBER: US/09/898,888
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/340,623
PRIOR PELIGNIO DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C
US-09-898-888-27545
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LOCATION: (1)...(532)
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US-09-053-375B-187
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Matches 636;
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Sequence 839, App
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-212-054-311
US-09-918-995-20569
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US-09-440-302B-839
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PCT-US02-24563-287
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39, Appl 39, Appl 39, Appl 287, App 287, App	
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ALIGNMENTS

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TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,3758
CURRENT FILING DATE: 1998-08-31
NUMBER OF ESO ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0 Sequence 187, Application US/09053375B GENERAL INFORMATION: APPLICANT: Chenchik, Alex 100.0%; S ilarity 100.0%; P Conservative 0;

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TYPE: DNA
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                                                                                                                                                              APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Marvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006CIP11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT FILIKG DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                           Sequence 839, Application US/09440302B GENERAL INFORMATION:
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Best Local Similarity
Matches 636; Conserv
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                                                                                1 GCCAGACCAAACCGGACCTCGGGGGGGGTGCGGGTGCTGCTGCTGCTGCTGCTCTCTC
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             TGCTGCAAGGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGTGGC
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies TITLE TELE REFERENCE: PTSJLCIN
CURRENT APPLICATION NUMBER: US/10/206,021
CURRENT FILING DATE: 2002-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.7%; Score 621.2; DB 6;
99.2%; Pred. No. 2.8e-138;
iive 3; Mismatches 1;
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                                                                                                                                                                                               Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 937
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                                                                                                                                                                                                                                                                                                                  Sequence 271, Application US/10206021 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (793)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Matches 631; Conserv
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LENGTH: 1273
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   264 gattacctagacattgtctgccccactacgaaggcccarggcccctgagggccccgag 323
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                                                                                     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG
                                                                                                                                               ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC
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                               ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCGTGCCAGGCAGAGGGCCCC
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: ROOM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
FILE REFERENCE: 20411-756
FILE REFERENCE: 20411-756
FILE REFERENCE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.1%; Score 357; DB 5; 98.4%; Pred. No. 1.8e-75; 1ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                 601 CITCIGATICITCGICTTCTGCGAATICTGTGAGCC 636
                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 20569, Application US/09918995; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(472)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-20569
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Matches 360; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-918-995-20569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 20569
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TGCTGCAAGGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGTGGC
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                                           ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PJZ1JC1N
CURRENT ENTING DATE: 2002-08-06
CURRENT FILING DATE: 2002-08-06
PIOR application removed - See File Wrapper or Palm
SOFFWARE: PETRY PARENT FILING DATE: 2.0
ENGYARE: PLOTE APPLICATION OF 2.0
SEQ ID NO 311
LENGTH: 1273
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NAME/KEY: misc_feature

LOCATION: (1069)

OTHER INFORMATION: n equals

US-10-212-054-311
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LOCATION: (793)
OTHER INFORMATION: n equals
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Matches 631; Conservative
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LOCATION: (782)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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; ORGANISM: HOMO US-10-212-054-1809
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US-10-212-054-1809
                                                       US-10-206-021-924
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Best Local Simi
Matches 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 gtggactggtcaggctacgaggcctgcacggcagaggggggaaatgccttccagcgctgg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 GIGCCCACTCCAGAGATTCIGGCCAGIGCTTGAGGCTCCCAGGIGTCTGTCTGCTGCAAG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 GAGAGGAAGTC----TGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 aggttgctccgaggagatgccgtggtggagctgggcttcaaccattacctagacatcttc
                                       571 AGCCCCCTCTGTCTCTTGCTATTACTGCTTCTGATTCTTCGTCTTCTGCGAATTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 317; DB 7; Length 48:
Pred. No. 5.9e-66;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                          APPLICANT: Abulin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sanda, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-333-9-05A
CURRENT APPLICATION NUMBER: US,10/142,593
CURRENT APPLICATION NUMBER: US 60/290,495
PRIOR APPLICATION NUMBER: US 60/290,495
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 352
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                    ; Sequence 207, Application US/10142593 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 49.8%; al Similarity 82.3%; 394; Conservative
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; ORGANISM: mus musculus
US-10-142-593-207
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tgagcc 387
                                                                                                                                                                                                                                       US-10-142-593-207
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Best Local (
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423 teegggtggeggggaggacaegegeeceageeeetgtgtetettgetgetgetgetget
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                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT251C1N
CURRENT APPLICATION WUMBER: US/10/206,021
CURRENT FILING DATE: 2002-07-29
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 937
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 924
LENGTH: 5831
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZ12C1N
CURRENT APPLICATION WUMBER: US/10/212,054
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2164
Prior application removed - See File Wrapper or Palm
SEQ ID NO 1809
LENGTH: 5831
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Pred. No. 4.3e-59;
0; Mismatches 4
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98.6%; Pred. No. 4.3e-59;
tive 0; Mismatches 4
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                                                                                                               Sequence 924, Application US/10206021 GENERAL INFORMATION:
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Best Local Similarity 98.6
Matches 291; Conservative
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US-10-206-021-924
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NOS: 325720
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Best Local Similarity
Matches 267; Conserv
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ORGANISM: Human
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SEQ ID NO 32020
LENGTH: 771
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                GGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACC
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42.0%; Score 267; DB 5; I
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
Matches 267; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-548
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/442,366A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: 09/053,375 PRIOR FILING DATE: 1998-03-31 NUMBER OF SEQ ID NOS: 2216 SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 548, Application US/09442366A
Sequence 548, Application US/09442366A
Sequence 548, Application US/09442366A
Sequence 548, Application US/09442366A
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENITON: Human Array
FILE REFERENCE: CLON-006CIP13
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LENGTH: 267
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Sequence 32020, Application US/10027632

Sequence 32020, Application US/10027632

GENERAL INFORMATION:
    APPLICAWT: Wang, David G
    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
    TITLE OF INVENTION: DAVID SOLVENTION: UNBER: US GOVIB: 006
    FRICHE REFERENCE: 12002-04-30
    CURRENT FILING DATE: 2002-04-30
    FRIOR FILING DATE: 2000-07-12
    FRIOR FILING DATE: 2000-07-12
    FRIOR FILING DATE: 2000-07-12
    FRIOR PRIOR NUMBER: US GO/193,483
    FRIOR FILING DATE: 2000-03-9
    FRIOR FILING DATE: 1999-11-23
    FRIOR FILING DATE: 1999-11-23
    FRIOR FILING DATE: 1999-11-23
    FRIOR FILING DATE: 1999-11-23
    FRIOR FILING DATE: 1999-10-03-03
    FRIOR FILING DATE: 1999-10-03-03
    FRIOR FILING DATE: 1999-10-03-03
    FRIOR FILING DATE: 1999-10-03-03
    FRIOR FILING DATE: 1999-00-03-03
    FRIOR FILING DATE: 1999-00-03-03
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    FRIOR FILING DATE: 1999-00-03-03
    FRIOR PRICEATION NUMBER: US GO/146,002
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    FRIOR PRICEATION NUMBER: US GO/146,002
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ilarity 100.0%; Pred. No. 4.3e-54;
Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/440,302B CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: 09/053,375 PRIOR FILING DATE: 1998-03-31 NUMBER OF SEQ ID NOS: 1193 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 242
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540 gaaggtgttcgtctgctgc 558
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LENGTH: 987
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APPLICANT: MUNGER, William E
APPLICANT: MUNGER, William E
APPLICANT: SALK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hisosh
APPLICANT: WAGA, Iwao
APPLICANTON: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
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                                                                           1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCTGCTGCGGGACTGTCCTC
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     Length 771;
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Best Local Similarity 54.3%; Pred. No. 4.1e-15;
Matches 271; Conservative 0; Mismatches 201; Indels 27
                                         Indels
     ;
     Score 143.4; DB 7;
Pred. No. 1.2e-24;
0; Mismatches 1;
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PCT-US02-25766-6624
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Best Local Similarity 99.3%;
Matches 144; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6624
LENGTH: 987
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 ---AGAGGGCCCCCGGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
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                            15 GACCTCGGGGGCGATGCGGCTGCTGCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT
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348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG
                                                                                                          AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT
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Pred. No. 4.1e-15;
0; Mismatches '201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE CANT: Bibliashvilli, Robert
TITLE PREFERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 186, Application US/09053375B GENERAL INFORMATION:
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Best Local Similarity 54.3%;
Matches 271; Conservative (
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Search completed: September 28, 2002, 01:35:28 Job time: 12728 sec
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Sequence 14, Application PC/TUSO213644

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth
TITLE OF INVENTION: Masahiko
TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene delivery
FILE REPERENCE: 6627-PA1198

CURRENT APPLICATION NUMBER: PCT/USO2/13644

CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                            4.1e-15;
                                               APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Neurobiology Array
FILE REFERENCE: CLON-006GTD11
CURRENT APPLICATION NUMBER: US/09/440,302B
CURRENT APPLICATION NUMBER: U9/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 1193
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 838
LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                              Score 103.4; Dred. No. 4.1e-0; Mismatches
             Sequence 838, Application US/09440302B GENERAL INFORMATION:
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Best Local Similarity 54.3%;
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo Sapiens
US-09-440-302B-838
·09-440-302B-838
                                                                                                                                                                                                                                                                                     TYPE: DNA
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201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 260
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                                                                                                                                                                                                                                                                      Length 1480;
                                                                                                                                                                                                                                                                      Score 101.8; DB 1; Length 1
Pred. No. 1e-14;
0; Mismatches 177; Indels
PRIOR APPLICATION NUMBER: 60/287,423
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | ||||| ||||| | |||| ggttgaaggtgactgtcagtggcaa 522
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.9%;
Matches 253; Conservative
                                                                                                                                                                       ; ORGANISM: Homo sapiens
PCT-US02-13644-14
                                                                                                                                                  TYPE: DNA
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September 27, 2002, 22:03:08; Search time 2180.79 Seconds (without alignments) 3936.217 Million cell updates/sec
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1 GCCAGACCAAACCGGACCTC......TTCTGCGAATTCTGTGAGCC 636
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4.5
Compugen Ltd.
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  GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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3356.8 3340.6 3340.6 3311.4 3211.4 3211.4 2231.4 252.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4 253.4

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W12777 BM258125 BF470931

AA296663 BJ074808 BJ031724

AW741367 BE234774 BI258895 AA002297

BF189993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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gb_htc:*
gb_gss:*
em_gss_hum:*
em_gss_inv:*

em_estro:* em_htc:* gb_est1:*

em_esthum:* em_estin:*

em_estba:*

EST:*

Database

em_estmu:* em_estov:* em_estpl:*

em_gss_vrt:*

SUMMARIES

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m	597	93.9	838	10	BE890843		601431292
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5	456.4	71.8	495	10	BG748489	BG748489	602706466
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7	440.4	69.2		10	BG338638	BG338638	602436387
80	414.4	65.2		10	BF792518	BF792518	602253627
6	404.2	63.6		10	BF138971	BF138971	601784106
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14	384.8	60.5		10	B1646617	BI646617	BI646617 603276523
15	378.8	59.6	565	σ	BE032073	BE032073 130886 MA	30886 MA
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	BI868252 6033920551 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402208 5', mRNA sequence. BI868252 FIREBESES I GI:16041925	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 912) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Emall: cgapbs-rémail.nih.gov Tissue Procurement: ATCC CONDA Library Preparation: Life Technologies, Inc.	H T T H	/clone_lib="NIH_MGC_90" //tissue_type="adenocarcinoma, cell line" //lab_host="DH108 (phage-resistant)" /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
RESULT 1 B1868252 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOORNAL COMMENT COMMENT SOURCE	RESULT 1 BI868252 LOCUS DEFINITION ACCESSION VERSION	SOURCE ORGANISM ORGANISM AUTHORS TITLE JOURNAL COMMENT	FEATURES	

ALIGNMENTS

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Conservative
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Best Local Similarity
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                   Gaps
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                                                                                   GCCAGACCAAACCGGACCTCGGGGGGGATGCGGCTGCTGCTGCTGCTGCGGGACTGTCCTC 71
                                                                                                                                              TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC
                                                                                                                                                                       GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAAGGGCCCCCTGAGGGCCCCCGAG
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                                 Score 622.4; DB 1
Pred. No. 9.9e-137
0; Mismatches 1
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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 264
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                                 97.98;
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BE890843

cDNA Library Preparation: Life Technologies, Inc

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM918 row, b column: 23

High quality sequence stop: 706.

Location/Qualifiers

1. 707

/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:3907510"
/clone="INAGE:3907510"
/lab_host="hHMCC."
/lab_host="bH10B (phage-resistant)"
/lab_host="OH10B (phage-resista
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Pred. No. 6.2e-134;
0; Mismatches 1;
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838 bp mRNA linear EST 20-OCT-2000 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916487 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                      /Organism="Homo sapiens"
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Salı; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                 Vertebrata; Euteleostomi;
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc/pcTpP
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lound through the I.M.A.G.E. Consortium/LINL at:
http://image.llni.gov.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 838)
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                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM9741 row: h column: 24
High quality sequence stop: 707.
Location/Qualifiers
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Best Local Similarity 98.1
Matches 625; Conservative
                              mRNA sequence.
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
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/ Clone="IRAGE: 4842011"
/ Clone="IRAGE: 4842011"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 bp mRNA linear EST 15-MAY-2001 602705246F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842011 5', mRNA sequence.
BG747752
EST 15-MAY-2001 5', BG747752.1 GI:14058405
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Note: this is a NIH_MGC Library. |"
167 c 144 g 103 t
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                                                                                                                                                                                                                                                                           61 TGGGCGGCGTTCCTCGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                            541 ACATCAGGGTGGCGA-GGGGGGACACTCCCAGCCCCCTCTGTCTTTGCTATTACTGCT 599
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High quality sequence stop: 493.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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human.
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us-09-904-954-3.rst

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BG748489 495 bp mRNA .linear EST 15-MAY-2001
602706466F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842977 5',
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://magqe.llnl.gov

Plate: LLCM1678 row: d column: 18

High quality sequence stop: 495.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
180
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/clone_Lib="NIH_MGC_43"
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                                                                           TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC
                                                                                                                                 GATTACCTAGACATTGTCTGCCCCCCACTACGAAGGCCCCAGGGCCCCCTGAGGGCCCCCGAG
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ORIGIN
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TITLE
JOURNAL
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AK012195 1255 bp mRNA linear . HTC 19-JAN-2002 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610529M21:ephrin A4, full insert sequence.
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Shono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishi,Y., Harama,M., Mishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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HTC; CAP trapper.
Hus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,
clone_lib:RIKB full-length enriched mouse cDNA library
clone:2610529M21.
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Hath-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9927923
Score 456.4; DB 1
Pred. No. 1.2e-97;
0; Mismatches 1
71.8%;
99.8%;
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AL Nature 409, 685-690 (2001)

Nature 409, 685-690 (2001)

Se (bases 1 to 1255)

RS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukudishi, Y., Furuno, M., Handarki, T., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Tawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tagama, T., Tejima, Y., Toya, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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83. 703
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SSHESAHPVGSPGESGTSGWRGGHAPSPLCLLLLLLPILRLLRVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, IWR:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                     4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Pred. No. 3.2e-94;
0; Mismatches 99; Indels 15;
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evidence:ISS
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1255
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374 c 357
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83. .703
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82.58;
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Best Local Similarity 82.5
Matches 537; Conservative
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BG338638 482 bp mRNA linear EST 27-FEB-2001 602436387F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554429 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                               61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
                                                                                                                                                                                                                                 121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
9
                                 GTGTCTGTCTGCTGCAAGGAGGAAGTC-----TGAGTCAGCCCATCCTGTTGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 TCAGAGAATTCAGCGCTTCACACTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG
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1 GCCAGACCAAACCGGACCTCGGGGGGGGGGATGCGGCTGCTGCCCTGCTGCTGCGGACTGTCCTC
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BG338638.1 GI:
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BG338638
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/db_xref="taxon:9606"
/clone=lib="NIH_MGE:1345734"
/clone=lib="NIH_MGE:1345734"
/clone=lib="NIH_MGE:1345734"
/tissue_type=adrenal cortex carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/note="Corgan: adrenal gland; Vector: pCWV-SPORT6; Site_1: Not1: Site_2: Sal1; cloned unidirectionally; oligo-dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9966 row: f column: 07
High quality sequence stop: 737.
High quality sequence stop: 737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 TGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGGAAGTCTGAGTCAGCCCATCCTGTTG
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                                                                                                                                                                                                                                                                                             sapiens"
      Ph.D.
    Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                      1. .751
/organism="Homo
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1. .482
/organism="Homo sapiens"
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MH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 TTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGCCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 CCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 440.4; DB 10; Length
Pred No. 7.4e-94;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 TCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 458
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BF792518
BF792518.1 GI:12097572
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6%;
Matches 452; Conservative
                                                                                                                                                                                                                                                                                                                                   Library."
161 c
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BI663095
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BI663095
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                                                                            Email: cgapDs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLAM9252 row: k column: 02
High quality sequence stop: 667.
I. 778
                                                                                                                                                                                                                                                                                                                                                           /tissue_type="tunor, metastatic to mammary"
/lab_host="DH10B"
/note="lorgan: lung, metastatic towv-SPORT6; Site_1: Not!;
Site_2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"
235 c 239 g 161 t
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               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AATGCCTTCCAGCGCTGGAATTGCTCGATGCCTTTTTGCCCCTTTCAGCCCTGTTCGATTC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 404.2; DB 10; Length 778;
Pred. No. 3.1e-85;
0; Mismatches 88; Indels 12;
                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Lu30"
                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                             /strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4012153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.6%;
Best Local Similarity 83.3%;
Matches 499; Conservative
   (bases 1 to 778)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
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to dT.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: Not1: Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: capabbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Length 1054;
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH108"
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Plate: LLAM11813 row: k column: 23
High quality sequence stop: 778.
Location/Qualifiers
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Pred. No. 2.7e-84;
0; Mismatches 96;
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/db_xref="taxon:10090"
/clone="IMAGE:5320846"
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82.4%;
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casas, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 561)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 11, 13, 15, 20,
                          351
                                                  382
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                                                                                                                                                      502
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                                                                       263 ACCTTTGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGCAGAGGGGGCA
                      472 GTGTCTGTCTGCTGCAAGGAGGAAGTC-----TGAGTCAGCCCATCCTGTTGGGAGC
                                                                                                                                                                                           CCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGGACACTCCCAGCCCCCTCTGTCTC
                                                                                                                                                                                                                                           ACTTACTACTACTACATCTCGGTGCCCACTCCAGAGATTCTGGCCCAGTGCTTGAGGCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                    AW784975 561 bp mRNA linear
115339 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW784975
                                                                                                                                                                                                                                                                                 TIGCTATIACTGCTGCTTCTGATICTTCG-TCTTCTGCGAATTCTGTGAGCC
                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .561
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 48 row: C column: 4
Seq primer: ATTTAGGTGACACTATAG.
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a 181 c
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AUTHORS
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KEYWORDS
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
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Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Laegreid, W. W., Rohrer, G.A., Chitko-MoKown, C.G.
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoml,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                              TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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                                                        Indels
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                   26;
     DB 9;
                           Pred. No 3.8e-84
0; Mismatches 5
  Score 399.4;
62.8%;
87.5%;
     Ouery Match 62.8
Best Local Similarity 87.5
Matches 463; Conservative
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us-09-904-954-3.rst

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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 85 row: N column: 6
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             61.6%;
87.2%;
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 and Keele, J.W.
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                                                                                  /db_xref="taxon:9913"
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/lab_host="Ple10B"
/note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled tissue from day 20 and day 40
embryos."
17 c 161 g 110 t
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                                                                                                                                                                                                                            Score 396.6; DB 10;
Pred. No. 1.7e-83;
0; Mismatches 69;
  FURNELLY STITCCCAGILALORD BACKWARD: GTTTTCCCAGILALORD BILD BALL 13 row: B COlumn: 13 Seq primer: ATTAGGTGACACTATAG. Location/Qualifiers
1.542
FORWARD: AGGAAACAGCTATGACCAT
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Best Local Similarity 85.4%;
Matches 457; Conservative
                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Sus scrofa
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
FORWARD: AGGAAACAGCTATGACCAT
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         normalized cDNA libraries for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 TCAGAGAAGATTCAGCGCTTCACACCCTTCTCCCTGGGCTTCGAGTTCTTGCCTGGAGAG 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGAGAGAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 392; DB 9;
Pred. No. 2.1e-82;
Design and use of two pooled tissue EST discovery in swine Unpublished (2000)
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      367
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/db_xref="taxon:10090"
/clone="IMAGE:5317037"
/clone="IMAGE:5317037"
/clone=Lib="NIH_CGAP_Mam3"
/tisue_type="tumor, gross tissue"
/lab_host="bull03"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
Technologies, catalog #12017-018. Investigators providing
Samples: Lothar Hennighausen/Chu-xia Deng, NIH Reference
for transgenic model: Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NII_CGAP Library."
                                                                                                                                                                                                                                                                                               Education Section Section Sections of Section Sections Sections Sections Sections Section Sect
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                                   BI646617 963 bp mRNA linear EST 12-SEP-2001 603276523F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5317037 5',
                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 CCAGGTTGCTTCGAGGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 TCTGCCCACATTATGAAAGCCCAGGGCCCCAGAAGGCCCGGAAACCTTTGCATTATAACA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 CCAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTACCTAGACATCT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 TCTGCCCCCACTACGAAGGCCCAGGGCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GGAATTTGCTCGATGCCTTTTTGCCCCTGTTCGATTCTCAGAAAGATTCAG 425
                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
"......" Entheria: Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 384.8; DB 10; Length
Pred. No. 1.3e-80;
0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 764.
Location/Qualifiers
1. .963
                                                                                                                         BI646617
BI646617.1 GI:15560853
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al Similarity 81.5%;
512; Conservative
                                                                                               mRNA sequence.
                                                                                                                                                                                                                        house mouse.
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
vo. 980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, N.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreld, W.W. and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for Growery in swine
Unpublished (2000)
Contact: Smith FPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                 545
                                                                                                                                                                                538
                     486
                                                                                                                                                                                                                                                                                          140 GGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCT 199
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                                                                                                              487 AAGGAGAGGAAGTC-----TGAGTCAGCCCATCCTGTTGGGAGCCCTGGAG--AGAGTG
                                                                                                                                                                                                                           546 AAGGAGAGCGGGTCATCACATGAGTCAGCTCATCCTGTTGGGAGTCCTGGAGCAAAAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE012073 Sorrofa CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4839
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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Best Local Similarity 87.6%; Pred. No. 2.8e-79;
Matches 429; Conservative 0; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
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1. .565
/organism="Sus scrofa"
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/clone_lib="MARC 1PIG"
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/lab_host="DH10B"
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 69. row: H column: 17
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BE032073.1 GI:8327082
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320 TGTGCTCCC-----TGCCCTTTGGCCATGTTCAGAGAAGATTCAGCGCT 370 [11111111]
255 AGTGCTCCCGCCCTTTGGTCCCTTTGGCCCTGTGCGGATTCTCAGAGAAGATTCAGCGCT 314
                                                                                                                                       AGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACATCAGGGT 550
                                                                                                                                                                                                                                                    551 GGCGAGGGGGGACACTCCCAGCCCCTCTGTTTGCTATTACTGCTTGTTGTTC 610
200 GCCCCCACTACGAAGGCCCAGGGCCCCTGAGGGCCCCCGAGACGTTTGCTTTGTACATGG 259
                                     260 TGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGGCCTACAAGCGCTGGG 319
                                                                         555 TGCGTCTCCT 564
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Search completed: September 27, 2002, 22:03:14 Job_time: 6600 sec

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Mouse EPH receptor

AAR94766

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September 28, 2002, 01:36:51; Search time 74.08 Seconds (without alignments) 301.375 Million cell updates/sec
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1091
1 MRLLPLLRTVLWAAFLGSPL......SPLCLLLLLLLLLLLRLRIL 201
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1; /grn.1
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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1. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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4. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
5. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
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9. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1980.DAT:*
110. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1980.DAT:*
121. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
122. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
123. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
124. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
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128. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
129. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:* 110... 111... 111... 112... 114... 116... 116... 116... 116...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human hek-L protei	Human AL-1, a liga	Lerk-7 protein. H	HEK4 binding prote	. Novel human diagno	Eph transmembrane	Human hek-L protei	Chicken EPH recept	Amino acid sequenc	Human PRO202 polyp	Human PRO202 prote
SUMMARIES		AAR97854	AAW02586	AAW00035	ABG27837	AAR82605	AAR71481	AAR94767	AAW71007	AAU12315	AAB50974
DB	16	17	17	17	22	16	16	17	19	22	22
% Query core Match Length DB I	201	228	228	228	335	234	238	200	200	204	204
% Query Match	100.0	34.9	34.9	34.9	34.9	33.6	33.4	32.9	32.9	31.4	31.4
Score	1091	380.5	380.5	380.5	380.5	366.5	364.5	359	359	343	343
Result No.	7	7	3	4	ស	9	7	80	σ	10	11

Amino acid sequence Human LERR-6 polyp Human PRO202 prote Human PRO202 prote Human PRO202 prote Bb1 protein sequence receptor bindi Lerk-6 protein. M Lerk-6 protein. M Lerk-6 protein. M Murine LERK-6 poly Truncated eck rece EPH receptor ligan Generic sequence f LERK-6 exon polype Amino acid sequence	AL-2-short (AL-2s) Human cytokine Ler NLERK2 ligand for EPH family ligand Human transmembran AL-2-long (AL-2l) Chicken Eph recept Ephrin-B2-Ephrin-B Mouse Eph receptor Murine hepatoma tr Drosophila melanog Drosophila melanog Drosophila melanog Evil length ligand		; tumorigenesis;
117 AANTOHOG 22 AAB50990 22 AAB50990 22 AAB50990 23 AAB50990 21 AAB50895 113 AAR53895 114 AAR53895 115 AAR53895 116 AAR6632 117 AAR91283 120 AAV66820 118 AAW18078 118 AAW18078 118 AAW18080 118 AAW18080 119 AAW11008 117 AAR91284 120 AAX96821 131 AAW18082 14 AAW11008 17 AAR91284 17 AAR91284	118 118 119 117 117 117 117	Protein; 201 AA. entry)	face; tyrosine kinase receptor; Location/Qualifiers 122 /note= "signal peptide" 23201 4WO-US09282. 3US-0109745. 3US-0161132. 4US-0240124. CORP. rretti DP;
31.4 31.4 31.5 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2 31.2		standard; ; 995 (first k-L protein	ensA. 95. 94; 9 93; 9 93; 9 94; 9 94; 9
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26-OCT-1995;
                                                                                          07-JUN-1995;
                              WO9613518-A1
                                                                                                    27-OCT-1994;
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                                                  09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                        Sequence
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  Domain
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                                                                                                                                                                                                                                                                                                                                         GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                   The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek seningen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL-1; REK7; eph-related tyrosine kinase receptor; ligand;
neurotrophic factor; neuropathy; anglogenesis; therapy; diagnosis.
                                      New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
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                                                                                                                                                                                                                                                DB 16; Length 201;
                                                                                                                                                                                                                                                                    0; Indels
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//label= Glycosylation
//note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "potential N-glycosylation site"
203.204
/label= GPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "potential attachment site for glycophosphatidyl-inositol"
                                                                                                                                                                                                                                               100.0%; Score 1091; DB 16; 100.0%; Pred. No. 8.5e-111;
                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR97854 standard; Protein; 228 AA.
                                                                                Claim 21; Page 38; 45pp; English
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        WPI; 1995-106811/14.
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                    N-PSDB; AAQ85888
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                                                                                                                                                                                                                  Sequence
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tyrosine kinase receptor REK7 (ARR97853). Its amino acid sequence was deduced from a cDNA clone (AAT18897) isolated from a human foetal brain. CDNA library. Recombinant, mature AL-1 can be produced in transformed host cells. It may be useful in promoting the development, maintenance or regeneration of neurons in vivo, and can be utilised in methods for the diagnosis and/or treatment of neurological disorders. It can also be used to promote or enhance anglogenesis. Antegonists and agonists of AL-1, as well as antibodies raised against AL-1, also have therapeutic applns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lerk-6; hek; elk; cell surface receptor; culture; reagent;
neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
Lerk-7; probe; cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 vemltlvflvlwmcvfsqdpgskavadryavywnssnprfgrgdyhidvcindyldvfcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLLL 200
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214..228
/label= Hydrophobic_domain
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                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caras IW, Winslow JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-239448/24.
N-PSDB; AAT18897.
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Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to modulate growth and differentiation of, e.g. liver and kidney cells, and to treat cancer and nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER4 and ECK receptors. Its amino acid sequence was deduced from a cDNA clone (AAT34292) isolated from a human placenta cDNA library. Expression vectors and host cells can be used for the prodn. of and/or differentiation of EPH sub-family receptor-bearing the growth esp. in liver, kidney, lung, skin or neural tissues. It can be used to treat neural system disorders and in the regeneration of damaged or depleted tissues. Antegonists are useful for cancer treatment. HEK4 BP can also be used to raise antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine kinase; ligand; growth; differentiation; cancer; nervous system disorder; therapy; antibody.
183 nslepaddtvhesaep----srgenaagtpripsrllaillfllamlltl 228
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                                                                                                                                                                                                                                       protein; HEK4 receptor; EPH-like
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20..228
/label= Mat_protein
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                                                                                        AAW00035 standard; Protein; 228 AA.
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                                                                                                                                                                                                                                     HEK4 binding
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                  24-OCT-1996
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Best Local Simi
Matches 88;
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                                                                                                                            AAW00035;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human Lerk-7 protein. Lerk-7 is predicted to be anchored to the cell surface via glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the exposed C-terminal amino acid of the processed mature protein, usually after cleavage upstream, often about 10-12 amino acids, of the N-terminus of the hydrophobic domain. Lerk-7 coding sequence (AAR132099) was isolated using a probe derived from the murine Lerk-6 DNA (AAR132700). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for adlivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human Lerk-7 cytokine - which binds to cell surface receptors elk, hek and eck, useful for delivering agents to cells or for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Gaps
                                                                                                                                                                                                                                   "C-terminal stretch of hydrophobic residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFSLGFEFLPGETYYXISVPTPESSGQ-CLRLQVSV-----CCK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%; Score 380.5; DB 17; Length 228; 38.3%; Pred. No. 3.5e-33; ive 32; Mismatches 75; Indels 35;
                                                                                                                                             1..133
/label= extracellular_receptor-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLRLRI 200
                                                                                                                                                                                                                                                                        /label= GPI_attachment_site
                                                                                                         1..228
/label= precursor_protein
                                                                    ...20
/label= signal_peptide
                                                                                                                                                                                                     spacer_region
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 37-38; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0396946.
                                                                                                                                                                                                                                                                                                                                                                                   95WO-US15781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                              134..183
/label= sp
194..208
/note= "C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-287171/29.
N-PSDB; AAT32699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AA;
                 Homo sapiens
                                                                                                                                                                                                                                                      Binding-site
                                                                                                                                                                                                                                                                                                            W09617925-A1
                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                    Peptide
                                                                                                         Protein
                                                                                                                                             Domain
                                                                                                                                                                                  Region
                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
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35;

Length 228;

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òγ

63

8

35; Gaps

Indels

75;

Mismatches

32;

Conservative

88;

Matches

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The candidectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) and its benefit antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Collagnostic amino acid sequences of the invention.

Collagnostic amino acid sequences of the invention.

Collagnostic amino acid sequences of the invention.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 58196; 103pp; English.
                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #27828
                                                                                                                                                                                         ABG27837 standard; Protein; 335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS92024
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001
                                                                                                                                                                                                                              ABG27837;
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                                                                                                                                                                       ABG27837
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Length 335;

Score 380.5; DB 22; Pred. No. 5.8e-33;

34.9%; 38.3%;

Best Local Similarity

Query Match

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Efl-2 (also known as EHK-IL) is an Eph transmembrane tyrosine kinase family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2 ends in a C-terminal hydrophobic sequence that appears to to be a recognition sequence allowing it to be GPI-linked and thus lacking in an intracellular domain. Efl-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in
             HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligands which bind Eph family receptors – used in the diagnosis of neurological disorders
                                                                                                     117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------
                                                                                                                                                                                                                                                                                                                                                   Ef1-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
neurological disorder; identification; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "residue borders main conserved regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldfarb M, Maisonpierre PC;
                                                                                                                                                                     155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRR 200
                                                                                                                                                                                                                                                                                                                           Eph transmembrane tyrosine kinase family ligand, Efl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "carboxy terminal hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPI-recognition tail
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                               AAR82605 standard; Protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gale N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US04208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                  16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-358635/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT03883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aldrich TH, Dar
Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9527060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-1994:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995
                                                                                                                                                                                                                                                                        AAR82605;
                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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Cheng H, Flanagan JG;
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 77; Conserv
                                                                               See also AAR71482.
                                                                                                                       238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT15009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9609384-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elf-1; EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR94767;
                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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    888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                   3;
promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
                                                                                                                                                                                                                                                                                                      ---GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRF 115
                                                                                                                                                                                                                                                                                                                                          68 ssgagpgpgggaeqyvlymvsrngyrtcnas--qgfkrwecnrphaphspikfsekfgry 125
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                     3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                              The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                   6
                                                                                                                                         DB 16; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine kinase receptor; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                        : ||||:|| | |||||| || :|||:| ||| safslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpv 174
                                                                                                                                                                                                                                                                                                                                                                                 116 TPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                 67;
                                                                                                                                     33.6%; Score 366.5; DB 1
45.6%; Pred. No. 1.2e-31;
Live 16; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "signal peptide"
20..238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR71481 standard; Protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0109745.
93US-0114426.
93US-0161132.
94US-0240124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beckmann MP, Cerretti DP;
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligand; cell surface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hek-L protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-106811/14.
                                                                                                                                                            Local Similarity
nes 77; Conserv
                                                                             234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ85887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR71481;
                                                                                 Sequence
                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                      63
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68 ssgvgpgagpgpggaegyvlymvsrngyrtcnas--qgfkrwecnrphaphspikfsek 125
                                                                                                                                                                                                                                                                                                                                                                                                                      -----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine and chicken EPH receptor ligand, {\rm Elf}\text{-}1 - useful in diagnosis and treatment of disorders associated with the {\rm Elf}\text{-}1 gene, e.g.
detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor ligand; dementia; tachycardia; therapy; transgenic animal.
                                                                                                                                                                                                                     Score 364.5; DB 16; Length
Pred. No. 2.1e-31;
5; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61..150
/label= Cys4_motif
33..157
/label= Core_sequence_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22..200
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 88-89; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR94767 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken EPH receptor ligand Elf-1.
                                                                                                                                                                                           33.4%; Scc.
44.5%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dementia, tachycardia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0308814,
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                                                                                                                                                                                                                                                                           77; Conservative
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06-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU12315;
                                                                                                                                                                                                                                Query Match
              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.
A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15009) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                 63 GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
                                                                                                                                                      Gaps
                                                                                                                                                                                       3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                     62; Indels 10;
                                                                                                                                                                                                                                                            120 LGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHPVGSPGES 170
                                                                                                                                                                                                                                                                         Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "contains a core sequence motif"
                                                                                                                               32.9%; Score 359; DB 17;
45.1%; Pred. No. 6.5e-31;
tive 23; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains a Cys4 motif" 35.157 /note="contain"
                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of an avian Elf-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
61..150
                                                                                                                                                                                                                                                                                                                                    AAW71007 standard; Protein; 200 AA.
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94US-0308814.
95US-0393462.
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                                                                                                                                                     78; Conservative
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                                                                                                                                           Best Local Similarity
                                                                                                 200 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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19-SEP-1994;
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                                                                                                  Seguence
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                                                                                                                                 Query Match
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The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek 4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 359; DB 19; Length 200; 45.1%; Pred. No. 6.5e-31; tive 23; Mismatches 62; Indels 10
1; Columns 75-78; 53pp; English.
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99US-0170262.
99WO-US30095.
99WO-US30911.
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2000WO-US00277.
2000WO-US00376.
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99WO-US28564
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Matches 78; Conserv
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09-DEC-1999;
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AAB50974 standard; Protein; 204
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PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of fonderocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS---- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
                                                                                                                                                                                                                                                                                                       Deforge L, Desnoyers L, Filvaroff E, G:
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.4%; Score 343; DB 22; Length 204; 38.7%; Pred. No. 3.7e-29;
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2000WO-US14042
                            2000WO-US04342
                                              2000WO-US04414
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Matches 79; Conservative
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Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                       Beresini M,
                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                            22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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10-NOV-2000;
                                                                                              01-MAR-2000;
20-MAR-2000;
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30-MAR-2000;
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                            18-FEB-2000;
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The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, covarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
                                                                                                                                      Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
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                                                                                                                                                            antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.
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Wood WI;
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99US-0140650.
99US-0141037.
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99WO-US20111.
99WO-US20594.
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99WO-US28313
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2000WO-US06319
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                                           (first entry)
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, Smith V,
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                                                                                        Human PRO202 protein.
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N-PSDB; AAC91576.
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18-FEB-2000;
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30-NOV-1999;
01-DEC-1999;
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Shelton DL,
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08-SEP-1999
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16-DEC-1999;
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AAB50974;
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treatment of disorders associated with the Elf-1 gene, e.g.
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S
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                                                                    11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP
                                                                                      ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG
                                                                                                                   128 ETYYYISVPTPESSGOCLRLOVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----
                                           26;
                            Length 204;
                                                                                                                                                                                                                                                              Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
diagnosis; transgenic animal.
                                           73; Indels
                                                                                                                                                                                                                                                                                                                                                                             'note- "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                     /note= "potential N-glycosylation
184
                            31.4%; Score 343; DB 22; 38.7%; Pred. No. 3.7e-29; ive 26; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                      15..166
|Tabel= Core_sequence_motif
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  'label Sig_peptide
                                                                                                                                                                                                                                                                                                                                  Mat_protein
                                                                                                                                                                                                   AAR94766 standard; Protein; 209 AA
                                                                                                                                                                                                                                                                                                                                       69..159
/label- Cys4_motif
                                                                                                                                                183 ----- 195
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177 sighsaaprlfplawtvlllplll 200
                                                                                                                                                                                                                                                 Mouse EPH receptor ligand Elf-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US11869
                                                                                                                                                                                                                                  (first entry)
                          Query Match
Best Local Similarity 38.7<sup>7</sup>
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                        21..209
/label- 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng H, Flanagan JG;
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      204
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                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                  02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1996
                                                                                                                                                                                                                  AAR94766;
      Sequence
                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                         Region
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Mouse; EPH receptor ligand; Elf-1; mek-4; sek-Ap; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 LNDYLDIVCPHYEGPGPP-EGPETFALYMYDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
                                                                                                A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15008) obtd. from an embryo mid- and hind-brain cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLPLLRTVLWAAFLGSPLRG-----GSSLRHVVYWNSSNPRLL-----RGDAVVELG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP
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35..166
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184
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "contains core sequence motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.4%; Score 342.5; DB 17;
42.5%; Pred. No. 4.4e-29;
live 20; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "contains a Cys4 motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 ift-snsscsglgg-----chlflttvpvl 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..20
/note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                   Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW71006 standard; Protein; 209
dementia, tachycardia , etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.59
Matches 90; Conservative
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AAB50990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                  The present sequence represents a mammalian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LEKR-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival (e.g. transplantation), also therapeutically in increase neuron survival nervous system and lymphatic tumours, to induce differentiation of hearboard properties to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury; cell proliferation; neural growth; neural tissue; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 llplillll-----plrarnedparanadryavywnrsnprfqvsavgdgggytvevs 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLPLLRTVLWAAFLGSPLRG-----GSSLRHVVYWNSSNPRLL-----RGDAVVELG 49
                                                                                                                                                                                           Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.4%; Score 342.5; DB 19;
42.5%; Pred. No. 4.4e-29;
live 20; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | || | ::|
180 ift-snsscsglgg-----chlflttvpvl 203
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ID AAY06822 standard; Protein; 213 AA
                                                                                                                                                                                                                                              Claim 1; Fig 2A; 53pp; English
                                                       95US-0455001.
94US-0308814.
95US-0393462.
                                 95us-0455001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human LERK-6 polypeptide.
                                                                                                        HARD ) HARVARD COLLEGE.
                                                                                                                                 Flanagan JG;
                                                                                                                                                        WPI; 1998-466665/40.
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Best Local Similarity
Matches 90; Conserv
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                                                                                                                                                                      N-PSDB; AAV42926
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                                                                     19-SEP-1994;
27-FEB-1995;
                                 31-MAY-1995;
                                                          31-MAY-1995;
          18-AUG-1998
                                                                                                                                 Cheng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                     ormation
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The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the hex or elk receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating meurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and also be used as carriers for delivering agents attached to cells bearing the elk or hex cell surface receptor. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 vevsindyldiycphygaplppaermehyvlymvngeghascd-hrgrgfkrwecnrpaa 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLL 195
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180 apepiftsnnscss--pgg-----crlf1stipv1_207
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neurodegenerative; excitotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 42; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                      98WO-US17772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
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Best Local Similarity
Matches 90; Conserv
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                                                                               Homo sapiens
                                                                                                                                                   WO9910495-A1
                                                                                                                                                                                                                                                                                                  27-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerretti DP;
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The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angiora, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue respeneration. The PRO nucleic acids, polypeptides and anti-PRO angiogenic disorder.
                              Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; vasotroplc; antitheumatic; antiarthritic; antiinflammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; angiogenic disorder; cancer; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                              99US-0141037.
99US-0144758.
99US-0145698.
99US-0146222.
                                                                                                                                                                                                                 17-MAY-2000; 2000WO-US13705
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99WO-US28313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders in a mammal
Human PRO202 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-025251/03.
N-PSDB; AAC90574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 AA;
                                                                                                                                                        WO200073445-A2
                                                                                            wound healing
                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
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15-MAR-2000;
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30-MAR-2000;
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20-JUL-1999
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30-NOV-1999
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71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
                                                                                               GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS---- 182
4 lwap11g1ccs1aaadrhtvfwnssnpkfrnedytihvq1ndyvdiicphyedhsvadaa 63
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Gaps

27;

11 LWAAFLGSPLRGGSSLRHVVWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70

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Query Match 30.8%; Score 335.5; DB 22; Length 205; Best Local Similarity 38.5%; Pred. No. 2.5e-28; Matches 79; Conservative 27; Mismatches 72; Indels 27;

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Sequence Sequence Sequence 1

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CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
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330.3
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US-08-240-124-4
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September 28, 2002, 01:37:42; Search time 29.18 Seconds (without alignments) 168.250 Million cell updates/sec
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                                                                                                                                                                                               1 MRLLPLLRTVLWAAFLGSPL......SPLCLLLLLLLLLLLRLRLRIL 201
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-048-129-2
US-09-048-079-2
US-08-486-449-4
PCT-US95-15781-5
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US-08-440-815-4
US-08-379-802-2
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US-08-308-814-2
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              version
- 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
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length: 2000000000
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1091
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                                                                                                                                                                 Title:
Perfect score:
Sequence:
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1091
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Sequence Sequence Sequence

US-08-448-736-1

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Sequence 1, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
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Patent No. 551668
CENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version 5.1a
US-08-441-216-2
US-08-452-779-1
US-08-299-567-4
US-08-445-065-1
US-08-959-524-1
US-08-959-524-1
US-08-959-524-1
US-09-173-133-2
US-09-173-133-2
US-09-173-133-2
US-09-175-1779-2
US-09-165-533-2
PCT-US95-12779-2
US-08-155-101-5
PCT-US95-11869-5
US-08-09-609-324A-8
US-08-09-609-324A-8
US-08-09-609-324A-8
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 1233-0644
INFORMATION FOR SEG 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: AMINO acid
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-240-124-4
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MOLECULE TYPE: protein
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US-08-453-943-4
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                                                                                                                                                                                                                                                                              121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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                                                                              Gaps
                                                                                                                                         1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                     Length 201;
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US-08-453-943-4
US-08-453-943-4
Sequence 4, Application US/08453943
Sequence 4, Application US/08453943
PAPLICANT: BECKNAMN, M. P.
APPLICANT: BECKNAMN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                            Indels
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COMPUTER SHIOL
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/240,124
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REFERENCE/DOCKET NUMBER: 2814-C
TELEPHONE: (206) 233-0644
TELEPHONE: (206) 233-0644
                                     100.0%; Score 1091; DB 1;
100.0%; Pred. No. 5.2e-116;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 UNIVERSITY STREET CITY: SEATLE STATE: WASHINGTON COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                        : 201 amino acids amino acids
                                   Query Match
Best Local Similarity 100.(
Matches 201; Conservative
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                           ;
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Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDS THE CELL SURFACE
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version 5.1a
100.0%; Score 1091; DB 1;
100.0%; Pred. No. 5.2e-116;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Maintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BI
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: (206) 233-0644

TELERAX: (206) 233-0644

NEDRAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09057121
Patent No. 5969110
                                                                                                                                                                                                                                                                                                                                                            181 PSPLCLLLLLLLLLLRLRIL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32
  Query Match
Best Local Similarity 100.0
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
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61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                             121 GFEFLPGETYYYISVPIPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                    GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                           Gaps
                                                                                                                                                                                                                      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
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                                                                                                                 Length 201;
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                                                                                                                                                           Indels
                                                                                                                 100.0%; Score 1091; DB 4;
100.0%; Pred. No. 5.2e-116;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 380.5; DB 1 Pred. No. 2.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Torchia, Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: 920C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08442248
Patent No. 5759863
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPLCLLLLLLLLLRLLRIL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 PSPLCLLLLLLLILRLLRIL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.9%;
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415/952-9881
                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                        ; MOLECULE TYPE: protein US-09-358-734-4
      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-442-248-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-442-248-4
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                                                                                                                                                                                              1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                  Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BECKMANN, M. P.
APPLICANT: BERETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
WIDMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: IMMUNEX CORPORATION
STREET: SEATTLE
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734
                                                                                                             Query Match 100.0%; Score 1091; DB 2; Best Local Similarity 100.0%; Pred. No. 5.2e-116; Matches 201; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/POCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09358734 Patent No. 6274117 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PSPLCLLLLLLLLLLRLLRL 201
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                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
  amino acid
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TYPE: am. TOPOLOGY:
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                                                      US-09-057-121-4
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60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122
                                                           1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP
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                                                                                                                                     183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILFELLAMLLTL 228
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                                       117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK----
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Ligands for EPH-Like Receptor NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.9%; Score 380.5; DB 38.3%; Pred. No. 2.8e-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09048129
Patent No. 6063903
                                                                                                                                                                                                                                                   Sequence 2, Application US/08379802
Patent No. 6057124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WINTER: ROBERT B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                             Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity
Matches 88; Conserv
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   Gaps
                                                           4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63
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                                       1 MRLLPLLRTVLW-AAFLGSPLRGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
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Patent No. 579848
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 460 Point San Bruno Blvd
CITT: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,7001
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38.3%; Pred. No. 2.8e-35;
Live 32; Mismatches 75
   Mismatches
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 32;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/922-9881
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/952-9881
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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 Conservative
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88; Conserv
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 88;
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Best Local Si
Matches 88;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,802
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Patent No. 6280732
                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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38.3%;
                                                                                                                                                                                                                                                                                                                         : 228 amino acids
amino acid
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Best Local Similarity 38.34
Matches 88; Conservative
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 COMPUTER READABLE FORM:
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                                                                                                                                FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228
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GENERAL INFORMATION:
THILE BATION:
TITLE OF INVENTION:
INVER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
STREET: California
               APPLICANT: Bartley, Timothy D.
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Ligands for EPH-Like Receptor NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 34.9%; Score 380.5; DB 3; Best Local Similarity 38.3%; Pred. No. 2.8e-35; Matches 88; Conservative 32; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                           US/09/048,129
                                                                                                               ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,802
FILING DATE:
                                                                                                                                                                                                      ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 228 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-048-129-2
                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                       SOFTWARE:
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60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 228;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno.Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 380.5; DB 4 
Pred. No. 2.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,449
FILING DATE: 06-JUN-1995
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, MOLECULE TYPE: protein US-08-299-567-5
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TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63
                                                                                                                                                                                                                                                                                                                                 DB 4; Length 228;
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                                                                                                                                                                                                                                                                                                                            ; Score 380.5; DB 4; Length 2; Pred. No. 2.8e-35; 32; Mismatches 75; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: PCT/US95/15781
FILING DATE: 05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated Lerk-7
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REPERENCE/DOCKET NUMBER: P0920P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-981
TELEFAX: 415/952-981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,025
FILING DATE: 06-DEC-1994
CLASSIFICATION:
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FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172 REFERENCE/DOCKET NUMBER: 2829-WO TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application PC/TUS9515781 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 34.9%;
38.3%;
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 38.35
Matches 88; Conservative
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ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                    35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                         : :| |: || | | | : || || || || || 4 VEMLILVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP
                                                                                                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 old Saw Mill River Road
CITY: Tarrytown
STRATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: PROBENTING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORREY/AGRNT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: REG 290
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK-
                                                                                                                                                                                                                                                                               Query Match 34.9%; Score 380.5; DB 5; Best Local Similarity 38.3%; Pred. No. 2.8e-35; Matches 88; Conservative 32; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08299567
Patent No. 5747033
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:.
LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 234 amino acids
amino acid
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                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-15781-5
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63 -----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                                                                                                                  68 SSGVGPGAGGGGGGGGGCYLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
  3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                            8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                        126 FQRYSAFSLGYEFHAGHEYYYISTPTHULHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                                                               112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
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                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08453943
Patent No. 5738844
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
COMMERS.POWDENCE ADDRESS:
ADDRESSED: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.4%; Score 364.5; DB 1; Best Local Similarity 44.5%; Pred. No. 1.9e-33; Matches 77; Conservative 16; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 238 amino acids
amino acid
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REGISTRATION NUMBER: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
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  Length 234;
                                                                                                                                                                                                                                                                116 TPFSLGFEFLPGETYYYISVPTPESSGOCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                                                                                                                          APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
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  DB 1;
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33.8%; Score 368.5; DB 1
45.6%; Pred. No. 6.7e-34;
tive 17; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/114,426
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KAPHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/240,124
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08240124
Patent No. 5516658
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 amino acids
                  Best Local Similarity 45.6
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-240-124-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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  Query Match
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                                                                       68 SSGVGPGAGGGGGGGGGYVLXMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
                                             63 -----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                            126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                  GERERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETT, DOUGLAS P.
APPLICANT: CERRETT, DOUGLAS P.
APPLICANT: CERRETT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.4%; Score 364.5; DB 2; Best Local Similarity 44.5%; Pred. No. 1.9e-33; Matches 77; Conservative 16; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
TELEX: 756822
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE:
                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09057121
Patent No. 5969110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 238 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WASHINGTO COUNTRY: 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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Search completed: September 28, 2002, 01:37:42 Job time: 10062 sec

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US-60-212-656-335 US-60-163-062-1186 US-60-185-360-275

Sequence 1232, App Sequence 335, App Sequence 335, App Sequence 4, Appli Sequence 5, Appli Sequence 2, Appli Sequence 15, Appli Sequence 16, Appli Sequence 15, Appli Sequence 16, Appli S

US-08-330-128-4 US-08-330-128-4 US-08-346-5 US-08-442-245-4 US-08-442-249-4 US-08-442-249-4 US-08-478-68-4 US-08-378-660-5 US-08-95-70-327-2 US-08-95-70-327-2 US-08-109-77-28-9 US-08-229-402-7 US-08-229-402-7 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-08-109-745-2 US-09-948-941-315-3 US-09-948-941-360-6 US-09-948-941-360-6 US-09-96-214-61-7 US-08-39-462-4 US-08-39-462-4 US-08-39-462-4 US-08-39-462-4 US-08-39-462-4 US-08-39-462-4 US-08-39-462-4 US-08-96-115-109-4 US-08-730-700A-15-108-0 US-09-621-55-13-108-0 US-09-9621-55-13-108-0 US-09-921-700A-16-0 US-09-927-796-40-1

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Sequence 4, Application PC/TUS9409282

Sequence 4, Application PC/TUS9409282

GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETIT, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MICROSOFT WORD SYSTEM 7.1 SOFTWARE: MICROSOFT WORD FOR APPLICATION DATA: APPLICATION NUMBER: PCT/US94/09282 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A A ADDRESS:
ADDRESS:
La: IMMUNEX CORPORATION
CITY: SEATULE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
MRUTER PT
VEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/114,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Si
                                                                                                                                                                                       44444600000444
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Sequence 17, Appl
Sequence 17, Appl
Sequence 1064, Appl
                                                                           (without alignments)
281.495 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                              September 28, 2002, 01:43:26 ; Search time 251.33 Seconds
                                                                                                         US-09-904-954-4
1091
1 MRLLPLERTVLWAAFLGSPL.....SPLCLLLLLLLLLLLLRLLRIL
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ptodata/2/paa/US099_COMB.pep:*
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'ptodata/2/paa/US098_COMB.pep:
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             US-09-904-954-4
US-09-214-631-8
US-08-730-700A-17
US-09-621-595-17
US-09-760-443-1064
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                                                                                                                                                                                      3502263 segs, 351980561 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-161-13
                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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/cgn2_6/
/cgn2_6/
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Match
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100.0
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                                           OM protein
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                                                                Run on:
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Sequence 48, Appl Sequence 288, App Sequence 2, Appli Sequence 2, Appli

US-09-135-129-2 US-08-393-462-2

ALIGNMENTS

Sequence 16, Sequence 40,

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61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRLLPLLRTVLWAAFLGSPLRGSSLRHVVYWNSSNPRLLRGDAVVELGENDYLDIVCPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BECKRANN, M. P.
CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,954
FILING DATE: 12-Jul-2001
CLASSIFICATION: CUNCOND
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1091; DB 5; 100.0%; Pred. No. 1.1e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/240,124
FILING DATE: 
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
                            NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEFX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SEESE, KATHRYN A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09904954 GENERAL INFORMATION:
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STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 201 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-161-132-4
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-904-954-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRLLPELKTVLWAAAFLGSPLRGSSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0\$; Score 1091; DB 1; Length 201; Best Local Similarity 100.0\$; Pred. No. 1.1e-101; Matches 201; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08161132
GENERAL INFORMATION:
APPLICANT: BECKHANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
TITLE OF INVENTION: RECEPTOR HEK
UNMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/161,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
APPLICATION NUMBER: US 08/109,745
                                                                                      ATTORNEY AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
METERY ACCOUNTY INFORMATION:
TELEPHONE: (206) 233-0644
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: IMMUNEX CORPORATION STREET: 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPLCLLLLLLILRELRIL 201
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                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: SEATTLE
STATE: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-161-132-4
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121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                   GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                               Sequence 17, Application US/08730700A
GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
TITLE OF INVENTION: Method of Activating a Novel Ligand
TITLE OF INVENTION: Regulatory Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATREET: 600 University Avenue
CITY: Toronto
STATE: 0ntario
COUNTY: Canada
21P: M5G 1X5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,700A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/005,518

FILING DATE: 13-0CT-1995

ATTORNEY/AGENT INFORMATION:

NAME: KURÓNYK, LINGA M.

REGISTRATION NUMBER: 34,971

REFERENCE/DOCKET NUMBER: 3153-196

TELECOMMUNICATION INFORMATION:

TELEPHONE: 416-586-3135

TELEFENA: 416-586-3110

INFORMATION FOR SEQ ID NO: 17:
                                                                                                                          181 PSPLCLLLLLLLLLRLLRIL 201
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                                                                                                  181 PSPLCLLLLLLLLILRLLRIL 201
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99.0%;
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amino acid
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Best Local Similarity 99.0°
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROOM 970
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US-08-730-700A-17
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SEGURAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Holland, Sacha
APPLICANT: Momanlu, Geraldine
APPLICANT: Momanlu, Geraldine
APPLICANT: MOMANLON: DIGGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS
TITLE OF INVENTION: UNABER: US/09/214,631
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: OCT/CA97/00473
EARLIER APPLICATION NUMBER: 60/021,272
MUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NOS: 13
SOFTWARE: PATENTIN VER: 2.0
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REFERENCE/DOCKET NUMBER: 2814-C
                                                                                                                                                                  ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-904-954-4
          TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFA: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          LENGTH: 201 amino acids TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 201; Conservative 0;
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US-09-214-631-8
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                                                                                   Gaps
                                             1;
  DB 11; Length 200;
                                             1; Indels
Score 1067.5; DB
Pred. No. 2.6e-99;
0; Mismatches 1
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or file wrapper

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NAME/KEY: SITE
LOCATION: (101)
OTHEN PRORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-760-443-1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 850; DB 21; Length 228;
Pred. No. 3.2e-77;
3; Mismatches 23; Indels
                  APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: 97212
CURRENT APPLICATION NUMBER: US/09/760,443
CURRENT FILING DATE: 2001-01-16
Prior application data removed - refer to PALM or file wrapp
NUMBER OF SEQ ID NOS: 2164
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1064
LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1232, Application US/60230435
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.98;
85.88;
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77.2%;
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Best Local Similarity 85.8%
Matches 157; Conservative
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Best Local Similarity 77.2
Matches 132; Conservative
                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: HUMAN
US-60-230-435-1232
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (152)
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217 PAP 219
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LENGTH: 964
                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 200;
                                                                                                                                                          Henkemeyer, Mark
TITLE OF INVENTION: Method of Activating a Novel Ligand
Regulatory Pathway
                                                                                                                                                                                                                                                                                                                                        COUNTY: Canada

ZIE: M5G 1X5

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPALIDLE

COMPUTER: IBM PC PC DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 21-Ju1-2000

CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.8%; Score 1067.5; DB ilarity 99.0%; Pred. No. 2.6e-99; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/730,700
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: KUTGYGYK, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-621-595-17
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Room 970
STREET: 600 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-760-443-1064
; Sequence 1064, Application US/09760443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 116-586-3135
TELEFAX: 416-586-3110
INFORMATION FOR SEQ ID NO: 17:
                                                                                                  Sequence 17, Application US/09621595 GENERAL INFORMATION:
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  180 PSPLCLLLLLLLLLRLRIL 200
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                                                                                                                                        APPLICANT: Pawson, Anthony
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 199; Conserv
                                                            RESULT 6
US-09-621-595-17
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Gaps

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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPRENCE: CLOO0768
CURRENT APPLICATION NUMBER: US/60/230,435
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 2991
                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                            Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFAL 75
                                                                                                                                                                                                                                                                                                                                                                    Length 964;
                                                                                                                                                                                                                                                                                                                                                                    DB 26;
                                                                                                                                                                                                                                                                                                                                                               Score 675.5; DB 26;
Pred. No. 8.6e-59;
3; Mismatches 21;
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Sequence 1186, Application US/60163062
GENERAL INFORMATION:
APPLICANT: BODAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: CL000134
CURRENT APPLICATION NUMBER: US/60/163,062
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1302
SEQ ID NO 186
SEQ ID NO 186
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.7%; Score 542; DB 26;
100.0%; Pred. No. 1.8e-46;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Caras, Ingrid W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRYE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/330,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Johnston, Sean A. REGISTRATION NUMBER: 35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-OCT CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 96; Conserv
                                                                                                 710 HSGEKPV 716
                                                                  158 SESAHPV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-60-163-062-1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                          RESULT 11
US-60-163-062-1186
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US-08-330-128-4
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TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
FITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000673
CURRENT APPLICATION NUMBER: US/60/212,656
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 795
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                     APPLICANT: BONDZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: BROODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO0287
CURRENT APPLICATION NUMBER: US/60/185,360
CURRENT FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 342
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 120
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712 LGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFAL 771
                                           76 YMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISV 135
                                                               98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKER 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 RLIRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                    -----HGCVRERGLVACDE--CEDRLPGASQREGDQSSQCHWH----PSP 870
                                                                                                                             136 PTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSG---WRGGDTPSP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.0%; Score 665; DB 26;
100.0%; Pred. No. 8.1e-59;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 600; DB 26;
Pred. No. 2.9e-51;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 335, Application US/60212656 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Sequence 275, Application US/60185360 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.0%;
Best Local Similarity 84.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: HUMAN
US-60-185-360-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: HUMAN
US-60-212-656-335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-212-656-335
                                                                                                                                                                                                                                      RESULT 9
US-60-185-360-275
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LENGTH: 776
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60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
                                                                                                                                                                                                               64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122
                                                                                                                                                                                                                                                                                                       123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182
                                                                                                                                 35; Gaps
                                                                                                               1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                     117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------
                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 228;
                                                                                                                                                                                                                                                                                                                                                 155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.9%; Score 380.5; DB 8
38.3%; Pred. No. 1.1e-29;
iive 32; Mismatches 75
                                   Score 380.5; DB 7
Pred. No. 1.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08440567
GENERAL INFORMATION:
APPLICANT: Garas, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,567
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,700
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TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
                                     34.9%;
38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Torchia, Timothy REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 228 amino acids
                                 Query Match
Best Local Similarity 38.35
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.99
Best Local Similarity 38.33
Matches 88; Conservative
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US-08-440-567-4
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8
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                                                                                                                                                                                                                                                                                                                                                                                        117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK------- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                       1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                           DB 7; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                                                                                                                                                                           ,1e-29;
.os 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATUS SYSTEM: System 7.1
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,946
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-396-946-5
Sequence 5, Application US/08396946
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated Lerk-7
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           34.9%; Score 380.5;
38.3%; Pred. No. 1.1e
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,025
FILING DATE: 06-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2829-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO 1D NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                         LENGTH: 228 amino acids
TYPE: amino acid
TOPOLOGY: linear
415/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 228 amino acids
amino acid
                                                                                                                                                                                                           Query Match 34.99
Best Local Similarity 38.33
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-396-946-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDAL.
STREET: Datary: Seattle
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TELEPHONE:
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HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
                    PFSLGFEFLPGETYYXISVPTPESSGQ-CLRLQVSV----CCK------- 154
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                                                                                                                                         155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,245A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                             US-08-442-245A-4; Sequence 4, Application US/08442245A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/330128
FILING DATE: 27-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: TOTChia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acids
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Best Local Similarity 38.34
Matches 88; Conservative
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Search completed: September 28, 2002, 01:43:27 Job time: 892 sec

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US-09-904-954-4
1091
1 MRLIPLLRTVLWAAFLGSPL.....SPLCLLLLLLLLLLIRLRIL 201
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                             September 28, 2002, 01:45:54
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:* Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:
3: /cgn2_6/ptodata/1/paa/USO7_NEW_COMB.pep: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Gaps

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Length 201; 3; Indels

Score 1073; DB 6; Pred. No. 2.4e-97; 0; Mismatches

Query Match 98.4%; Best Local Similarity 98.5%; Matches 198; Conservative

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1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

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	0138	Sacha Geraldine Tony Tony BY TRANSMEMBRANE LIG TYROSINE KINASES 7.23USWO MUMBER: US/10/138,787 202-05-03 MBER: US/09/214,631 999-03-12 MBER: VCT/CA97/00473 999-07-04 MBER: 60/021,272 996-07-05 : 13 er. 2.0
20000000000000000000000000000000000000	US/1	acha Geraldine Coraldine COOMERIZ PEROSINE TYROSINE TYROSINE 2002-05- 1003-03-12 199-03-12 199-03-12 195-07-04 18ER: 6070 195-07-05
NANNANNANNANNANÄÄÄÄ	87-8 87-8 Application US/10138787	ANT: HOLland, Sacha ANT: Holland, Geraldine ANT: Pawason, Tony OF INVENTION: OLIGOMERIZED RECEPTY OF INVENTION: OLIGOMERIZED RECEPTY OF INVENTION: DY TRANSMEMBRANE L OF INVENTION: BY TRANSMEMBRANE L OF INVENTION: TYROSINE KINASES THERENCE: 11757.23USWO OF INVENTION: TYROSINE KINASES TAPPLICATION NUMBER: US/10/138,7 T FILING DATE: 1999-03-12 APPLICATION NUMBER: PCT/CA97/0047 FILING DATE: 1999-03-12 APPLICATION NUMBER: PCT/CA97/0047 FILING DATE: 1996-07-05 FILING DATE: 1998-07-05 FIL
	Cat	MATION: Olland, Mbamalu Pawson, Pawson, ENTION: ENTION: CE: 117 CCE: 117 CC
	ppl	HECKMATION: Mbamalu INVENTION: IN
	87-8 8, A	NECKLOND TO THE TRANSPORT TO THE TRANSPO
	RESULT 1 US-10-138-787-8 ; Sequence 8, Applicat	APPLICANT: HOLland, Sacha APPLICANT: HOLland, Sacha APPLICANT: HOLland, Geraldi APPLICANT: Pawson, Tony TITLE OF INVENTION: BY TRAN TITLE OF INVENTION: TYROSIN FILE OF INVENTION NUMBER: USPRIOR APPLICATION NUMBER: USPRIOR PLING DATE: 1999-03-11 PRIOR FILING DATE: 1996-07-0 PRIOR FILING DATE: 1996-07-0 NUMBER: PAPLICATION NUMBER: OF PRIOR FILING DATE: 1996-07-0 NUMBER OF SEQ ID NOS: 13 SOFTWARE: PALENTIN VET. 2.0 LENGTH: 201 LENGTH: 201 TYPE: PRI ORGANISM: HOMO SAPIENS -1797E: PRI ORGANISM: HOMO SAPIENS
78888888884444444444444444444444444444	ULT 10-1 eque	APPLICA APPLICA APPLICA APPLICA TITLE TITLE TITLE FUREN FUREN PRIOR ONTHERE EQ ID LENGT LE
	RESULT US-10-	S

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Sequence 9, Application US/10138787
GENERAL INFORMATION:
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85.8%;
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Best Local Similarity 38.3%
Matches 88; Conservative
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                        Best_Local Similarity 85.8
Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              PSP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 PAP 219
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                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (101) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LUCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-206-021-615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (101)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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Sequence 1064, Application US/10212054

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ212C1N

CURRENT APPLICATION UMBER: US/10/212,054

CURRENT FILING DATE: 2002-08-06

NUMBER OF SEQ ID NOS: 2164

Prior application removed - See File Wrapper or Palm

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 850; DB 6; Length 228;
Pred. No. 2.3e-75;
Sequence 615, Application US/10206021
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT251CIN
CURRENT APPLICATION NUMBER: US/10/206,021
CURRENT FILING DATE: 2002-07-29
PILIA APPLICATION TEMOVED - See File Wrapper or Palm ·
NUMBER OF SEQ ID NOS: 937
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.9%;
85.8%;
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Matches 157; Conservative
                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PSP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 PAP 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                            FEATURE:
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NAME/KEY: misc_feature
LOCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
LOCATION: (159)
                                                                                                                                           ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-212-054-1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOMMALU, GECHALDING
APPLICANT: MOMMALU, GECHALDING
APPLICANT: MOMMALU, GECHALDING
APPLICANT: PAWSON, TONY
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: TYROSINE KINASES
FILE REPERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR APPLICATION NUMBER: 60/021,272
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-07-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- 154
                                                                                                                                                                                                                                                                                                                                                                       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                           Length 228;
                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                        Score 850; DB 6; L
Pred. No. 2.3e-75;
3; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.8%; Score 379.5; DB 6; 38.3%; Pred. No. 4.1e-29; ive 32; Mismatches 75;
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ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 IMAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES ANI TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION NUMBER: BCODING THE SAME CURRENT APPLICATION NUMBER: BCT/US02/24563

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR FILING DATE: 1997-08-17

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-19

PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | :| | | :| SIGHSAAPRLFPLAWTVLLLPLLL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 ----- 195
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 38.79
Matches 79; Conservative
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Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: HOMO
PCT-US02-24563-288
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APPLICANT:
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                                                                                                                                                                                                                                                                                               APPLICANT: Mommalu, Geraldine
APPLICANT: Mammalu, Geraldine
APPLICANT: Mammalu, Geraldine
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757_201500
CURRENT PAPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR APPLICATION NUMBER: 60/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1996-07-04
PRIOR FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13
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          123 PFSLGFEFPPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 SSGAGPGGGGAE-YVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEKFORY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 233;
                                                                                        183 NSLEPADDIVHESAEP----SRGENAAQTPRIPSRLAILLFELAMLLTL 228
                                                           ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TPFSLGFEFLPGETYYYISVPTPESSGOCLRLQVSVCCKERKSESAHPV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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GENERAL INFORMATION:
APPLICANT: Holland, Sacha
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Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
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Smith, Victoria
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Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US02-24563-288
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Desnoyers, Luc

APPLICANT: Elivaroff, Ellen

APPLICANT: Good, Wal-Olang

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Smith, Victoria

APPLICANT: Sherwood, Steven

APPLICANT: Shewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: And APPLICANT: Saniel

APPLICANT: Shory School N.

APPLICANT: APPLICANT: Saniel

APPLICANT: APPLICANT: Shory School N.

APPLICANT: Shory School N.

APPLICANT: 
                             APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: 105/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                                                                                                                                                                                                                                                   Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 288
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EQ ID NO 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 343; DB 6;
Pred. No. 1.4e-25;
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Watanabe, Colin K
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Best Local Similarity 38.7%
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US-10-121-049-288
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; ORGANISM: Homo Sapien
US-10-121-050-288
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330ARLC23
CURRENT APPLICATION NUMBER: US/10/121, 053
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                                 64 EQYILXLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122
                                                                                                                                                                                                      71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
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                                                                                                                                 4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63
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  Length 204;
                                                  Indels
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31.4%; Score 343; DB 6; 38.7%; Pred. No. 1.4e-25;
                                                  26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 288, Application US/10121053 GENERAL INFORMATION:
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Smith, Victoria
Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
Query Match
Best Local Similarity 38.77
Matches 79; Conservative
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US-10-121-053-288
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APPLICANT: Gav Wei-Oiang
APPLICANT: Garitsen, Mary E.
APPLICANT: Garitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: ALANGA, Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Alang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C4
CURRENT APPLICATION NUMBER: US/10/121, 047
CURRENT FILING DATE: 2002-04-11
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
                                                                                                      APPLICANT: Watanabe,Colin K
APPLICANT: Watanabe,Colin K
APPLICANT: Watanabe,Colin K
APPLICANT: Watanabe,Colin K
APPLICANT: Wandy, Zenn
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING, THE SAME
FILE REFERENCE: P3330R1C5
CURRENT APPLICATION NUMBER: US/10/121,044
CURRENT FILING DATE: 2002-04-11
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 288
LENGTH: 204
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ilarity 38.7%; Pred. No. 1.4e-25;
Conservative 26; Mismatches 73.
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                                                                Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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  Gurney, Austin L.
                       Sherwood, Steven
Smith, Victoria
                                                                                          Tumas,Daniel
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Best Local Similarity
Matches 79; Conserv
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US-10-121-047-288
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TTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330RIC15
CURRENT APPLICATION NUMBER: US/10/121,043
CURRENT APPLICATION TOWNER: US/10/121,043
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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177 SIGHSAAPRLFPLAWIVLLLPLLL 200
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Goddard, Audrey
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Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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Best Local Similarity 38.78.
Matches 79; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
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Filvaroff, Ellen
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Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-121-043-288
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APPLICANT: Wood,William
APPLICANT: Zhag, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C25
CURRENT APPLICATION NUMBER: 105/10/121,056
CURRENT FILING DATE: 2002-04-12
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                                                                                                                          183 ----- 195
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177 SIGHSAAPRLFPLAWIVLLLPLLL 200
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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Gurney, Austin L.
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Filvaroff, Ellen
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Matches 79; Conservative
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SEQ ID NO 288
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US-10-121-056-288
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APPLICANT GOOWER'S LUC
APPLICANT GOOWSKI, PAUL ST.
APPLICANT GOOWSKI, PAUL J.
APPLICANT GOOWSKI, PAUL J.
APPLICANT GOOWSKI, PAUL J.
APPLICANT SHEWOOD, SLEWEN ABELICANT SHEWOOD, SLEWEN APPLICANT SHEWOOD, SLEWEN APPLICANT SHEWOOD, SLEWEN APPLICANT STEWART, TIME THE APPLICANT TUMBS, DAIL APPLICANT WOOD, MILLIAM APPLICANT SOOT, MILLIAM APPLICANT SOOT, MILLIAM APPLICANT SERVET SENDING THE SAME TILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TILLE REFERENCE: P3330RICH APPLICATION NUMBER: US/10/121,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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                                                                                                                                                                                                                       73; Indels
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                                                                                                                                                        ; DB 6;
1.4e-25;
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                                                                                                                                                        Score 343;
Pred. No. 1
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Best Local Similarity 38.75
Matches 79; Conservative
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SEQ ID NO 288
                          ; ORGANISM: Homo Sapien
US-10-121-047-288
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US-10-121-054-288
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APPLICANT: GLOWSKI, PAUL J.
APPLICANT: GLOWSKI, PAUL J.
APPLICANT: Sherwood, Steeven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanab
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Best Local Similarity 38.7%; Pred. No. 1.4e-25;
Matches 79; Conservative 26; Mismatches 73; Indels 26; Gaps
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Gao, Wei-Oiang
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo Sapien
US-10-121-057-288
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APPLICANT:
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Search completed: September 28, 2002, 01:45:54 Job time: 619 sec

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OM protein - protein search, using sw model

Run on: September 28, 2002, 01:38:54; Search time 49.23 Seconds

(without alignments) 392.321 Million cell updates/sec US-09-904-954-4

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		đ			SUMMARIES	
Result		Query				
NO.	Score	Match	Length	DB	QI	Description
1	1091	100.0	201	7	I38850	LERK-4 - human
7	380.5	34.9	228	7	158170	LERK-7 precursor -
3	373	34.2	228	7	A57084	·H
4	364.5	33.4	238	7	I38849	LERK-3 - human
5	346.5	31.8	213	7	JE0322	ephrin-A2 - human
ø	342.5	31.4	209	7	A54984	ELF-1 protein prec
7	334.5	30.7	205	7	A36377	B61 protein precur
80	164.5	15.	336	7	149766	hepatoma transmemb
თ	156	-	333	7	I84743	hepatoma transmemb
10	146	13	346	7	S46993	elk ligand - human
11	145	13	345	7	158406	LERK-2 - rat
12	144		345	~	148780	Stral/Eplg2 protei
13		12.1	462	7	T32645	$\overline{}$
14	113	10.		7	T19914	hypothetical prote
15	87	8.0	628	~	I38000	О
16	82		164	7	F87296	hypothetical prote
17	82	•	268	7	S24377	
18	84		325	7	I65354	stem cell antigen
19	ã	•	385	7	152565	stem cell antigen
20	83.5	7.7	577	П	VGBEGI	glycoprotein E - s
21	83	7.6	198	7	G42148	GTP-binding protei
22	ന	7.5	206	7	A84664 ·	probable phytocyan
23	80.5	7.4	564	7	153106	gene gli protein -
24	80	7.3	351	~	I54347	rod outer segment
25	80	7.3	351	~	168620	rod outer segment
26	80		472	~	AG3600	cellulose synthase
27	79	7.2	278	~1	C84266	hypothetical prote
28	~	7.1	620	7	T30765	hypothetical prote
29	77.5	7.1	248	7	H70027	carboxylesterase h

N;Alternate names: AL-1 C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999 C;Accession: 158170; G01812 R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P Neuron 14, 973-981, 1995

RESULT 2 158170 LERK-7 precursor - human

	nypornerical prote hypothetical prote	gene APXL protein	transcription fact	2Pl precursor - mo	transcription fact	transcription fact	transcription fact	probable phytocyan	nicotinic receptor	GTP-binding protei	Delta-4 protein -	alpha-2-macroglobu	nonstructural prot	titin - rabbit (fr
B64783	T22641	137183	S10099	146382	A34734	C34734	B34734	H84715	T01378	A45384	JC7570	T43166	S38480	S20901
7	7 (7	7	7	7	7	4	4	~	7	7	7	7	7	7
261	310	1616	582	623	654	742	825	200	502	219	685	1503	2115	6805
7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	6.9	6.9	6.9	6.9	6.9
77.5	77.5	77.5	77	77	77	77	77	76.5	9/	75.5	75.5	75.5	75.5	75.5
30	32 32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en A;Reference number: 138849; MUID:95140419
A;Accession: I38850
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                    C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
                                                                                                                                                                                                                    A) Status: preliminary; translated from GB/EMBL/DDBJ.
A) Molecule type: mRNA
A) Residues: 1-201 <RES>
A) Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YEGPGPPEGPETFALXMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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                                                                                                                                                                                                                                                                                                                                                A,Gene: GDB:EPLG4
A,Cross-references: GDB:438337; OMIM:601380
A,Map position: 1q21-1q22
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Best Local Similarity 42.1%.
Matches 91; Conservative
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A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved A;Reference number: I58170; MUID:95267434
A;Accession: I58170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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6
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R.Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K. submitted to the EMBL Data Library, May 1995
A.Reference number: G08477
A.Reference number: G08477
A.Stocession: G01812
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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llarity 38.3%; Pred. No. 1.7e-28;
Conservative 32; Mismatches 75;
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88; Conserva
                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-228 <RES>
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Best Local S:
Matches 87
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Best Local S
Matches 88
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C;Species: Homo sapiens (man)
C;Daccession: 138449
B;Rozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S
C,Nocogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs
A;Reference number: I38849; MUID:95140419
A;Accession: I38849
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
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C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0329
C;Accession: JE0329
C;Accession: JE0329
C;Accession: JE0329
C;Accession: JE0329
C;Accession: JE0322
A;Reference number: JE0322; MUID:99045414
A;Reference number: JE0322; MUID:99045414
A;Retexion: JE0322
A;Status: preliminary
                                                                                 A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 -----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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                                                                                                                                                                                            201
                                                                                                                                                                156 RKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLLLLLLRLLRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.8%; Score 346.5; DB 242.1%; Pred. No. 2.5e-25; ive 21; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.4%; Score 364.5; DB Best Local Similarity 44.5%; Pred. No. 5.7e-27 Matches 77; Conservative 16; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule, type: mRNÅ
A;Residues: 1-213 -AAS>
A;Cross-references: GB-AJ007292; NID:9368836
C;Superfamily: axon guidance signal protein
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A. 10 May 1

IVCPH	A; Title: A novel immediate-early response gene of endothelium is induced by cytokines A; Reference number: A36377; MUID:91042512 A; Accession: A36377 A; Status: preliminary A; Molecule type: mRNA
OY 102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159	5 <hol> es: GB:M57730; GB kon guidance signa</hol>
Qy 160 SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLL 195  1	Query Match 30.7%; Score 334.5; DB 2; Length 205; Best Local Similarity 38.5%; Pred. No. 3.3e-24; Matches 79; Conservative 27; Mismatches 72; Indels 27; Gaps 6;
	OY 11 LWAAFLGSPLRGGSSLRHVVWWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70             ::       :
LE-1 protein preduxsor - mouse  N.Alternate names: Cek7 ligand C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: II-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999 C;Accesion: Asiana	OY 71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFBFLP 126   :     :     :     :     :
R;Cheng, H.J; Flanagan, J.G. Cell 79, 157-168, 1994 A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the	OY 127 GETYYISVPTPESSGQCLRLOVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS 182   :        :       :
A; Neterior number: A34504; MULD:930U///O A; Accession: A54984 A; Status: preliminary A; Molecule type: mRNA	Qy 183PLCLLLLLLLL 195
A; Residues: 1-209 <che. 11="" 1995="" 270,="" 3467-3470,="" a="" a.;="" a55873;="" a;="" and="" b;="" biol.="" cdna="" cek7="" characterization="" chem.="" cloning="" cross-references:="" d.a.;="" dixit,="" gb:u14941;="" h.;="" j.="" kinase="" l.;="" lou,="" m.f.;="" muid:95181289<="" nid:9558836;="" number:="" of="" pandey,="" pid:9558837="" pidn:aaa53636.1;="" protein-tyrosine="" receptor="" reference="" shao,="" siever,="" td="" title:="" v.m.="" verderame,=""><td>RESULT 8 149766 hepatoma transmembrane kinase ligand - mouse C.Species: Mus musculus (house mouse)</td></che.>	RESULT 8 149766 hepatoma transmembrane kinase ligand - mouse C.Species: Mus musculus (house mouse)
	C;Date: U.Jul. 149766 R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matth Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995 A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine A;Reference number: 149766; MUID:95199254 A;Accession: 149766
Query Match 31.4%; Score 342.5; DB 2; Length 209; Best Local Similarity 42.5%; Pred. No. 5.8e-25; Matches 90; Conservative 20; Mismatches 67; Indels 35; Gaps 10;	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-336 <res> A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678 C;Genetics:</res>
OY 3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELG 49	. 0.7
Qy 50 LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGH 105	Conservative 24
QY 106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163	Db 19 LAVLCRTAISRSIVLEPIYWNSSNSKFLPGGGLVLYPQIGDKLDIICP 66 Qy 60 HYEGPGPPEGPETALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFS 119
OY 164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLL 195	67 KVDSKTVGQ-YEYYKVYMVDKDQADRCTIKKENT-PLLNCARPDQDVKFTIKKQEFSPNL
DBT	OY 120 LGFEFEPGETYTYSTYTENSGQCLALQVSYCCKEESAHPVGSPGESGFEGGWGGD 1/9  121
RESULT 7 A36377 B61 protein precursor – human C:Species: Homo sapiens (man)	Oy 180 TPSP 183 
C;Decter: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999 C;Accession: A33377 R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.	

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 09-Mar.1996 #sequence_revision 09-Mar.1996 #text_change 05-Nov-1999
C; Accession: 138000; S51663
R; Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A; Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin A; Reference number: 138000; MUID:95296337
A; Accession: 138000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-628 <RES>
A; Cross-references: EMBL:X83425; NID:g603559; PIDN:CAA58449.1; PID:g603560
A; Note: parts of this sequence, including the amino end of the mature form, were conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                     Submitted to the EMBL Data Library, November 1996
A;Reference number: 219195
A;Recession: T19914
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-237 <WILD
A;Cross-references: EMBL:282262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.1
A;Experimental source: clone C43F9
C;Genetics:
                                                                                                                                                                                                                                                   hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19914
R;Mortimore, B.
---FSEKIORFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 SDETGK---YEYSYIYMVSDEEYDHCFLSKPRLV--GACDNQTINASINIVFRSFTPTPG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 LE---SHSREVIRCA-PEGTAEKVLRTQQLSGGRREDWKKQKVPPKNVAQLIRQLNPIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNP--RLLRGDAVVELGLNDYLDIVCPH
                                                                                                                       121 GFEFLPGETYYYISVPTPESSG------QCLRLQVSVCCKERKSESAHP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87; DB 2; Length 628;
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113; DB 2;
Pred. No. 0.0032;
6; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lutheran blood group glycoprotein precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:LU
A;Cross-references: GDB:120155; OMIM:111200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.48;
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88 AEGPRAYKRWV -- CSLPFGHVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GFEFLPGETYYYIS 134 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 32/2; 96/3; 214/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||| ||: |: ||
112 GFEFQPGKNYFLIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 19q12-19q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C: Keywords: glycoprotein F:1-31/Domain: signal sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: C43F9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                           207
                                                                                                                                                                                                                RESULT
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                                                                          ...... retalences: EMBL:AF038619; PIDN:AAB92075.1; GSPDB:GN00022; CESP:F56A11.3 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F56A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 HDYYITS--TSNGSLEGLENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TVKTATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSKVALFAAVGAGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPETFALYMVDWPGYESCQAE-GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEGPGPPE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 VLTLCRLATPL---AKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQ 87
                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-89, T', 91-345 <SHA>
A;Cross-references: GB:U12983; NID:9575928; PIDN:AAA53231.1; PID:9575929
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 13.2%; Score 144; DB 2; Length 34:
Best Local Similarity 24.5%; Pred. No. 5.9e-06; .
Matches 62; Conservative 28; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T32645
R; Gattung, S.; Goela, D.; Harper, M.
submitted to the EMBL Data Library, December 1997
B; Description: The sequence of C. elegans cosmid F56All.
A; Reference number: Z31204
A; Accession: T32645
A; Accession: T32645
A; Molecule: preliminary; translated from GB/EMBL/DDBJ
A; Molecule: type: DNA
A; Residues: 1-462 cGAT>
A; Cross-references: EMBL: AF038619; PIDN: AAB92075.1; GSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:F56A11.3
A;Map position: 4
A;Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3
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              A Status: preliminary
A Molecule type: DNA
A Residues: 1-345 <FLE>
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version 4.	- 2000
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

September 28, 2002, 01:48:24; Search time 27.02 Seconds (without alignments) 288.032 Million cell updates/sec Run on:

US-09-904-954-4 1091 Title: Perfect score: Sequence:

1 MRLLPLLRTVLWAAFLGSPL.....SPLCLLLLLLLLLLLRLLRIL 201

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P52798 homo sapien	mus n	snm 8		P52803 homo sapien		-			gal		hod	_					_	035393 mus musculu	Q15768 homo sapien	_			-		P52796 rattus norv	_	P47806 mus musculu	P50895 homo sapien	_	_	P08354 pseudorabie	P35291 rattus norv
SUMMAKIES		QI	EFA4_HUMAN	EFA4_MOUSE	EFA5_MOUSE	EFA5_RAT	EFA5_HUMAN	EFA2_BRARE	EFA5_CHICK	EFA5_BRARE	EFA3_HUMAN	EFA2_CHICK	EFA2_MOUSE	EFA2_HUMAN	EFA1_MOUSE	EFA1_HUMAN	EFA1_XENLA	EFA1_RAT	EFA3_MOUSE	EFB2_BRARE	EFB3_MOUSE	EFB3_HUMAN	EFB2_MOUSE	EFB1_XENLA	EFB2_HUMAN	EFB1_CHICK	EFB1_HUMAN	EFB1_RAT	EFB1_MOUSE	GLI1_MOUSE	_	CD34_MOUSE	MAT1_COCEL	VGLE_PRVRI	RB16_RAT
		DB				٦									٦			٦															-		-
		Length		206	228	228	228	195	228	228	238	200	209	213	202	202	216	205	187	332	340	340	336	327	333	334	346	345	345	1111	628	382	378	577	198
de			100.0	82.4	35.2	35.2	34.9	34.5	34.2	33.5	33.4	32.5	31.4	31.2	30.8	30.7	29.7	29.3	27.2	16.9	15.9	15.5	15.1	14.3	14.3	13.8	13.4	13.3	13.2	8.1	0.8	7.7	7.7	7.7	7.6
		Score	1001	898.5	383.5	383.5	380.5	376	373	365.5	364.5	355	342.5	340.5	336.5	334.5	324.5	319.5	296.5	184	173.5	169.5	164.5	156	156	151	146	145	144	88.5	87	Φ	m m	83.5	ď
	Result	No.		7	Э	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q63942 rattus norv	Q03393 nomo sapien P32958 mus musculu	P35276 mus musculu	P75713 escherichia	Q13796 homo sapien	P15923 homo sapien	Q05941 rattus norv	Q9nr61 homo sapien	Q28281 canis famil	P08641 gallus gall	P16443 rattus norv
RB3D_RAT	ROM1_HUMAN	RB3D_MOUSE	YLBA_ECOLI	APXL_HUMAN	TFE2_HUMAN	ACH7_RAT	DLL4_HUMAN	ARRS_CANFA	CAD1_CHICK	DBP_RAT
Н,		П	-	Н	<del>,</del> 4	٦	-	Н	-	-
219	351	219	261	1616	654	502	685	405	887	325
7.6	 	7.1	7.1	7.1	7.1	7.0	6.9	6.9	6.9	6.8
82.5	90	77.5	77.5	77.5	77	92	75.5	75	75	74.5
34	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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DR EMBL; U14188; AAC50079.1;		50
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use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch).	use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch).	use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ
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1	1	707

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Query Match
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                                   or send
                                                                                                                                                                      SIGNAL
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EFA5_MOUSE
                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
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                                                                                                                                                                                           ö
                                                                                        N-LINKED (GLCNAC. . ) (POTENTIAL).
SESAHPWESBGESGTESGENGENGLLLLLLILIL
LRIL -> NLPSHPKEPESSOPLEEGSLLPALGVPIQTD
KME (IN SECRETED ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                   61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPEGHVQFSEKIQRFTPFSL 120
                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                             MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97060319; PubMed=8903354;
Ribentiken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
Flientiken and overlapping expression patterns of ligands for
Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                         EFA4_MOUSE STANDARD; PRT; 206 AA.
008542; 055218;
01-Nov'1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephilin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerretti D.P., Nelson N.; "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3), mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6): conservation of intron/exon structure."; Genomics 47:131-135(1998).
                                                                                                                                                                                                                                                                                                    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                           ö
                                                                                                                                                                   Length 201;
                                                                                                                                                                                           Indels
                                                        Signal; Alternative splicing
                                                                                                                                    ABE8D5443A9AF28D CRC64;
                                                                                                                                                                  Score 1091; DB 1;
Pred. No. 1.6e-94;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                              EPHRIN-A4
                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98126446; PubMed-9465306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFNA4 OR EPLG4 OR LERK4 OR EPL4.
                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                               181 PSPLCLLLLLLLLLRLLRIL 201
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                                                                                                                                    ¥
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
                                ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1. Glycoprotein; GPI-anchor; Si
                                                                                                                                                                                        Conservative
                                                                     201
33
201
201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                 201 AA;
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                        Matches 201;
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                                                                                       CARBOHYD
VARSPLIC
                                                                                                                                   SEQUENCE
                                                                                                                                                                   Query Match
Best Local 3
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                                                                  SIGNAL
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EFA4_MOUSE
                                                                              CHAIN
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INDICES COMPARTMENTALIZED SIGNALING WITHIN A CAYBOLAE-LIKE
MEMBRAND MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
THE FYN TYROSINE KINASE (BY SIMILARITY).
-i- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSL---PFGHVQFSEKIQRFTP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRLLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFA5_MOUSE STANDARD; PRT; 228 AA.
008543; 008544;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
  as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . ) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN )
                        and for
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
EPHRIN-A 4.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ر.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G., "Distinct and overlapping expression patterns of ligands for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                           Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43501971DD1C6EA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.3e-76;
; Mismatches 22
                 modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 898.5;
non-profit institutions as long
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                                                                                                                                                  EMBL; U92890; AAC39962.1; -.
EMBL; U92889; AAC39962.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-97060319; Pubmed-8903354;
                                                                                                                                                                                                                                                           PRINTS; PRO1347; EPHRIN.
PRODOM; PRO0233; BPHRIN; 1.
PROSTTE; PSO1299; BPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6;
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EFNA5 OR EPLG7 OR LERK7 OR EPL7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22861 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%;
                                                                                                                                                                                     MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                  EMBL; U90663; AAB50238.1; -. EMBL; U92890; AAC39962.1; -.
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206
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 170; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  26
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Caras I.W.;

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228 AA;
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Best Local Similarity
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                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Matches
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FCPHYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQ 119
EPHB1 (BY SIMILARITY).
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 LFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVND 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 VCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Gaps
                                                                                                     K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRLLPLLRTVLW-AAFLGSPLRGGSSL---RHVVYWNSSNPRLLRGDAVVELGLNDYLDI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
                                                                    MICRODOMAINS (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 RFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN-A5.

N-LINKED (GLCNAC. . .) (POTENTIAL)

MISSING (IN SHORT ISOFORM).

85439F5337420022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLLRT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.2%; Score 383.5; DB 1;
Best Local Similarity 39.1%; Pred. No. 1.2e-28;
Matches 91; Conservative 31; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-95267434; PubMed=7748564;
MADLINE-95267434; PubMed=7748564; Shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26339 MW;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U90664; AAB50239.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 U90665; AAB50240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:107444; Efna5.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LERK-7) (AL-1).
EFNAS OR EPLG7 OR LERK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 1
228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFA5_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155
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C STRAIN-SPRAGUE-DAWLEY;

AL Y.Y., MCTiernan C.F., Feldman A.M.;

LI Y.Y., McTiernan C.F., Feldman A.M.;

Submitted (MAR-1998) to the FMBL/GenBank/DDBJ databases.

Submitted (MAR-1998) to the FMBL/GenBank/DDBJ databases.

INDUCES COMPATEMENTALIZED SIGNALING WITHIN A CAVEDLAE-LIKE

MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS

COGNATE RECEPPOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF

THE FYN TYROSINE KINASE (BY SIMILARITY).

C -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT

IS COMPATEMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE

MCRODOMAINS (BY SIMILARITY).

C -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.

C -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal. SIGNAL 1 \\ 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FCPHYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 VCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 RFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV----CCK----- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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ID EFAS_HUMAN STANDARD; PRT; 228 AA.

DE P52803;

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 10-0CT-2001 (Rel. 40, Last annotation update)

DT 16-0CT-2001 (Rel. 40, Last annotation update)

DE Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRLLPLLRTVLW-AAFLGSPLRGGSSL---RHVVYWNSSNPRLLRGDAVVELGLNDYLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-A5.
N-LINKED (GLCNAC. . .) (POTENTIAL).
855985532D580022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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      Beck K.D., Carastyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of AL-1, a ligand for an Eph-related receptor involved in axon bundle formation."; Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 N-
26358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U69279; AAC05801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP
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                                                                                                                                                                                                                                                                                                                    Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
"LERK-7: a ligand of the Eph-related kinases is developmentally
regulated in the brain.";
Cytokine 9:540-549(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHBI.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Davy A., Gale N.W., Murray E.W., Klinghoffer R.A., Soriano P., Feuerstein C., Robbins S.M.;
"Compartmentalized signaling by GPI-anchored ephrin-A5 requires the Fyn tyrosine kinase to regulate cellular adhesion.";
Genes Dev. 13:3125-3135(1999).
-I- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                    SEQUENCE FROM N.A. MEDLINE-95267434; PubMed-7748564; MEDLINE-95267434; PubMed-7748564; Minslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong Tsal S.P., Goddard A., Henzel W.J., Hefti F.; "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved in axon bundle formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.9%; Score 380.5; DB 1; Length 228;
                                                                       Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG-VAR_012035.
6893B1CCACFF3F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 34.9%; Score 380.5; DB 1; Best Local Similarity 38.3%; Pred. No. 2.2e-28; Matches 88; Conservative 32; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN-A5.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20069483; Pubmed-10601038;
                                                                                                                                                                                                                                                                                                  MEDLINE-97392664; PubMed-9245480;
                                                 Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26297 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00812; Ephrin; I. PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; I. PROSITE; PS01299; EPHRIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U26403; AAB60377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001799; Ephrin.
 (AL-1).
EPLG7 OR LERK7.
                                                                                                                                                                                                                                Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
228
37
55
                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 AA;
                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICRODOMAINS
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601535;
(LERK-7)
EFNAS OR 1
                                                                                                                                                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
                    axon growth and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADED FASHION THROUGHOUT THE TECTUM.
                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
9EE284FEB61D0C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
MEDLINE=97195707; PubMed=9043080;
Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
Bonhoeffer F., Holder N.;
                                                                                                                                                                           183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228
                                                                                                                                                       ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLLLLLLRLRI 200
                                                                          117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV----CCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Two Eph receptor tyrosine kinase ligands control axon be involved in the creation of the retinotectal map in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                           195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EPHRIN-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cypriniformes; Cyprinidae; Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y09668; CAA70863.1; -. ZFIN; ZDB-GENE-990415-66; efna2. InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Development 124:655-664(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            (LERK-6) (ELF-1) (ZFEPHL3).
EFNA2 OR EPLG6 OR LERK6.
                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00812; Ephrin; 1 PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zebrafish.";
                                                                                                                                                                                                                                                                                           EFA2_BRARE
P79727:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                    RESULT 6
EFA2_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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Gaps

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Indels

1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP

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No. 1.1e-27;

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Ω
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                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                  Gaps
                                                                                                                                                           26 RHAVYWNSSNSRFWQGEYTVAVSINDYLDVYCPYYESPQPHSRMERYILFMVNHDGYLTC 85
                                                                                                                       RHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda M., abhobefter F.;
Bun vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal protein related to ligands for Eph receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 82:359-370(1995).
-!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL GANGLION CELL AXONS.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                145 PCLKLKVYV----KPTSSGYESPEPFLTDQSQRCGADGP---CLAVLMLLLVFLL 192
                                                                                                                                                                                                                                                                                                                                                                            144 -CLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                              12;
Length 195;
                                                              57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ) (P
56D8E4FBDECF18AD CRC64;
; DB 1;
4.8e-28;
34.5%; Score 376; DB
45.7%; Pred. No. 4.8e
:ive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN-A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Posterior tectum;
MEDLINE=95360980; PubMed=7634326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 EF
228 EF
37 N-
26206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X90377; CAA62027.1;
                             Best Local Similarity 45.7
Matches ,80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LERK-7) (RAGS protein). EFNA5 OR RAGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFA5_CHICK
P52804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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34.2%; Score 373; DB 1; Length 228;

Query Match

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ZFIN; ZDB-GENE-980526-186; efna5b.
InterPro; IPROUJ799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PROSTITE; PS01299; EPHRIN.
DROSTITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION OF THE RETINO-TECTAL MAP.
                                                                                                                                                            PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV----CCK------E 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may
                                                                                                                                       HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
-!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE
FECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
OF THE TECTUM.
                               Gaps
                                                                                      Ephrin-AS precursor (EPH-related receptor tyrosine kinase ligand 7) (LERK-7) (AL-1) (ZEPBHL4).

EFRAS OR EFNASB OR ALI OR EPLG7 OR LERK7.

EFNASB OR ALI OR EPLG7 OR LERK7.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Two Eph receptor tyrosine kinase ligands control axon growth and
be involved in the creation of the retinotectal map in the
                                                                   1 MRLLPLLRTVLWAAFLG-SPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP
                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
Bonhoeffer F., Holder N.;
                                 Indels
                                                                                                                                                                                                                                                                                                       156 RKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLLLLLRLRIL 201
                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              228 AA
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=97195707; PubMed=9043080;
38.5%; P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 124:655-664(1997)
           Best Local Similarity 38.59
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            EFA5_BRARE
P79728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zebrafish.
                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
EFA5_BRARE
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us-09-904-954-4.rsp

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EMBL; L40932; AAC42229.1; -.
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       DOR NO DO
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8
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                                                                                                                                                                                                                                                                                                                                                119 SLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK-------- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE-95140419; PubMed-7838529;
Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
Cerretti D.P., Beckmann M.P.;
Ligands for the receptor tyrosine kinases hek and elk: isolation of
cDNAs encoding a family of proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELULAR LOCATION: Attached to the membrane by a GPI-anchor.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
                                                                                                                                                                                                                               3 LLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                            6 MIVFVGVILWMCVFSQEPSSKVMADRYAVFWNRTNPRFQRGDYHIDVCINDYLDVYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis S., Goldfarb N., Aldrich T.H., Maisonpierre P.C., Lhotak V., Pawson T., Goldfarb M., Yancopoulos G.D.; "Lignads for EPH-related receptor tyrosine kinases that require membrane attachment or clustering for activity."; science 266:816-819().
                                                 (POTENTIAL).
                                                                                                                                                                                  31;
                                                                                                                                        Length 228
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERKSESAHPV-GSPGESGTSGWRGGDTPSPLCLLLLLLLLLLLLL198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (174B3406C05418E6E CRC64)
                                                                                                                                                                                  75;
                                                                                                                                      DB 1;
                                                                                                                                      33.5%; Score 365.5; DB 38.2%; Pred. No. 5.4e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA
                                                                                                                                                                                  33; Mismatches
    POTENTIAL.
                       EPHRIN-A5
                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95063919; PubMed=7973638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LERK-3) (EHK1 ligand) (EHK1-L).
EFNA3 OR EPLG3 OR LERK3 OR EFL-2.
20 PC
228 EF
37 N-
26595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
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                                                                                                                                                                                  86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOOD LEUKOCYTES
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFA3_HUMAN
P52797;
                                            CARBOHYD
                                                                                                                                        Query Match
                                                                                                                                                             Best Local
                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 -----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVGPGAGPGPGGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 82:371-381(1995).
--- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND EPHA5 (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; "Complementrary gradients in expression and binding of ELF-1 and Mek4 in development of the topographic retinotectal projection map."; cell 82:371-381(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last sequence update)
Sphrin-A2 Drecursor (EPH-related receptor tyrosine kinase ligand 6)
(LERF 6) (ELF-1)
EFNAZ OR EFLG6 OR ELF1
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE TECTUM
                                                                                                                                                                                                                                                        . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 FQRYSAFSLGYEFHAGHEYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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-!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE PEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
N-LINKED (GLCNAC. .) (POT
MISSING (IN REF. 2).
W; BEFDGAEBFE33FDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      33.4%; Score 364.5; DB : 44.5%; Pred. No. 7.1e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                     POTENTIAL.
EPHRIN-A3.
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                                                                                                                                                                             Glycoprotein; GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                             26350 MW;
                                          Interpro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN. Procom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
L37360; AAA52368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.5%
The conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                             238
38
67
100
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67
100
71
                          601381;
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CARBOHYD
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1.
1.
Signal.
                                                                EMBL; U14941; AAA53636.1; --
EMBL; U14752; AAA68520.1; --
MGD; MGI:102707; Efna2.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRODOM; P0002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                               23586 MW;
                                                                                                                                                                                                                                      Glycoprotein; GPI-anchor; SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.59
Matches 90; Conservative
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170
184
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38
170
184
209 j
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shao H., Lou L., Pandey A., Verderame M.F., Slever D.A., Dixit V.M.; "CDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mex 4 and Sek receptor protein-tyrosine kinases."; J. Biol. Chem. 270:3467-3470(1995).
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                  3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                           65
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                                                                                                                                                                                                                                                                                                                                                                                                          10 LAAIVGVCVWSDDPGKVI----SDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIYCPHYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SWISS WEBSTER; TISSUE=Brain; MEDLINE=95007776; PubMed=7522971; Cheng H.J., Flanagan J.G.; "Identification and cloning of ELF-1, a developmentally expressed ligand for the Mek4 and Sek receptor tyrosine kinases."; Cell 79:157-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 39, Last sequence update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand (LERK-6) (ELF-1) (CEK7-Ligand) (CEK7-L).
                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
8FAB1AESE45EED96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 LGFEFLPGETYYYISV-PTPESSGQCLRLQVSV-CCKERKSESAHPVGSPGES 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%; Score 355; DB 1; Length 200; 45.1%; Pred. No. 4.5e-26; tive 22; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
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InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
PRODOM; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
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                                                                                                                                                                                                                                      23049 MW;
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                 22
200
36
161
175
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFA2_MOUSE
P52801;
                                                                                                                                                                        CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LLPLLRTVLWAAFLGSPLRG-----GSSLRHVVYWNSSNPRLL-----RGDAVVELG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98126446; PubMed-9465306;
Cerretti D.P., Nelson N.;
Cerretti D.P., Nelson N.;
Cerretti D.P., Nelson N.;
Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6);
conservation of intron/exon structure.";
Genomics 47:131-135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFA2_HUMAN STANDARD; PRT; 213 AA.
15-080.20;
15-080-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-INTINGATE (EPH-related receptor tyrosine kinase ligand (LERK-6) (HEK7-119and) (HEK7-E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.4%; Score 342.5; DB 1; Length 209; 42.5%; Pred. No. 6.8e-25; Live 20; Mismatches 67; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (PN N-LINKED (GLCNAC. . .) (PN N-LINKED (GLCNAC. . .) (PN F1997545F25B9ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLL 195
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
EPHRIN-A2.
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Giannotti J., Caruso A.,

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Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for
Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).

-!- SUBNOTIC: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
         Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1) (LERK-1) (Immediate early response protein B61).
EFNAL OR EPGLI OR LERKI OR EPLI.
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                            Takahashi H., Ikeda T.; "Mode T.; "Adecular cloning and expression of rat and mouse B61 gene: "Implications on Organogenesis."; Oncogene 11:879-883(1995).
                                                                                                                                                                                                                                                   Morris J.C., Clarletta A., Morris G.E., Glannotti J., Ce
Hammett D.J., Finnerty H., Turner K., Wood C.R.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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                                                                                                                                                 MEDLINE-95405853; PubMed-7675446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, D38146; BAA07344.1; -.
EMBL, U26188; AAA67563.1; -.
EMBL, U90662; AAB50237.1; -.
MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01347; EPHRIN.
ProDom; PD002533; EPHRIN; 1.
PROSITE; PS01299; EPHRIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23802
                                                     Mus musculus (Mouse).
                                                                                                                     SEQUENCE FROM N.A. STRAIN-ICR;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                          STRAIN-BALB/C;
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SIGNAL
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELGLNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SL 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLPLLRTVLWAAFLGSPL-----VGGSSLRHVVYWNSSNPRLLRGDA----V 45
                                                                                                                    11 SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
                                                                                                                                                SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> A (IN REF. 3).
RA -> PP (IN REF. 3).
AA -> RR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                               the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.2%; Score 340.5; DB 1; Length 213; 41.7%; Pred. No. 1.1e-24; ive 21; Mismatches 66; Indels 39
                                                              "Cloning, chromosal mapping, and tissue expression of the encoding the human Eph-family kinase ligand ephrin-A2."; Biochem. Blophys. Res. Commun. 252:378-382(1998).
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33C9FB1A8168B2D0 -CRC64;
                                                                                                                                                              (Potential).
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLL 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFA1_MOUSE STANDARD; PRT; 205 AA P5279; P97331; 01-007-1996 (Rel. 34, Created) 01-007-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-A2
                                                                                                                                                                                                                                                                                                       EMBL; U92896; AAC39577.1; -.
EMBL; U92893; AAC39577.1; JOINED.
EMBL; AQC8844; AAC39577.1; JOINED.
EMBL; AC004258; AAC04896.1; -.
EMBL; AJ007292; CAA07435.1; -.
MIM; 602756; -.
                                                   MEDLINE-99045414; PubMed-9826538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
hes 90; Conservative
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42
174
188
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25
29
213 AA;
                          SEQUENCE FROM N.A.
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                                       rissue-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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Glycoprotein; GPI-anchor; Signal
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205 A
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                                                                                                                  CARBOHYD
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                                                         SIGNAL
                                                                                          CHAIN
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                                                         <u>ن</u>
                                                                                                                                                                                                                                              71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
                                                                                                                                                                                                                                                                                      | :||||| | : || : || : || : || : || CHSYYISKPIYHQESQCLKLKVTVNGKITHNPQAHV--NPQEKRLQADDPEVQVLHSIG 180
                                                                                                                                                                                                                                                                                                                                                                                 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGES-------GTSG 174
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                                                            Gaps
                                                                                                                  11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
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01-MAR-2002 (Rel. 41, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
(LERK.1) (Immediate early response protein B61) (Tumor necrosis
factor, alpha-induced protein 4).
EFNAI OR EFGLI OR LERKI OR TNFAIP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holzman L.B., Marks R.M., Dixit V.M.;
"A novel immediate-early response gene of endothelium is induced by Act novel immediate-early response gene of endothelium is induced by Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-95140419; PubMed-7838529;

Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases hek and elk: isolation of
cDNAs encoding a family of proteins.";
Oncogene 10:299-306(1995).

--- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
--- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
--- INDUCTION: BY TWF-ALPHA AND INTERLEWININ-1 BETA.
--- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                         19;
                                                         Indels
Pred. No. 2.4e-24;
          39.8%; Preu. ....
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MEDLINE-91042512; PubMed-2233719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WRGGDTPSPLCLLLLLLLL 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M57730; AAA58388.1; -.
                                                  80; Conservative
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                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                       Best Local
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-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A.;
"Embryonic expression of eph signalling factors in Xenopus.";
Mech. Dev. 57:133-144(1996).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE XINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 MEQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand 1)
                                                                                                                                                                                                                                                                                                                                                                   4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                .) (POTENTIAL).
                                                                                                                                                                                           30.7%; Score 334.5; DB 1; Length 205; 38.5%; Pred. No. 3.7e-24; Live 27; Mismatches 72; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00812; Ephrin; 1.

PRINTS; PR01347; EPHRIN.

Probom; PD00253; Ephrin; 1.

PROSITE; PS01299; EPHRIN; 1.

Glycoprotein; GPI-anchor; Alternative splicing; Signal.
SIGNAL.
                           EPHRIN-A1.
N-LINKED (GLCNAC. . .) (P
. 4FEFC6BF4C1251A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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POTENTIAL.
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                    205 EF
26 N-
23771 MW;
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                                                                                                                                                                                                                                                                Conservative
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EFNA1 OR EPGL1 OR ELF.
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NCBI_TaxID=8355;
                                                                                               AA:
                                                                                                                                                                                                                              Best Local Similarity
Matches 79; Conserv
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29 216 EPHRIN-A1. 36 36 N-LINKED (GLCNAC. ) (POTENTIAL). 162 216 TPPPVNVHTPRCHIQSDEDEVPLEGVMKGVAGNGAAPGTPC TLYGLLLAALLIRL -> SE (IN ISOFORM A'). 216 AA; 24755 MW; 1B3A508E0A7B872E CRC64;	Query Match Best Local Similarity 39.7%; Pred. No. 3.3e-23; Matches 83; Conservative 25; Mismatches 66; Indels 35; Gaps 9;	11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY-EGPGPPEG 69	LWLREAQGERHIVFWNSSNYRFWQEDYTVQVQLNDYLDIVCPYYEEGSVAGHT 73	70 PETFALYWVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLP 126	FLVDYEEYETCKPKS-KDQVRWECNKPFAPHGPEKFCEKFQKFTPFTLGTEFRE 132	ESSGOCLRLQVSVCCKERK	GRIYYYISKPIHYHGETCMRLRVHVSGRTTPPPVNVHTPRSHIQSDEPEVPLPGVMKSVA 192	171 GTSGWRGGDTPSPLCLLLLLLLLLRL 197	193 GNSAAPGTPCTLYGLLLAALLIRL 216
, , ,	imilarity ; Conserva	FLGSPLRGGSS	LREAQG	ALYMVDWPGYE	rrelvoyeeye	YISVPTPESS	RTYYYISKPIHYHG	WRGGDTPSPLC	APGTPC
CHAIN CARBOHYD VARSPLIC SEQUENCE	Query Match Best Local Similarity Matches 83; Conserv	11 LWAAI	21 LW	70 PETE	74 VERY	127 GETY	133 GRTY)	171 GTSG	193 GNSA
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Search completed: September 28, 2002, 01:48:25 Job time: 639 sec

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044516 caenorhabdi

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September 28, 2002, 01:47:36; Search time 79.86 Seconds (without alignments) 435.412 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1091
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Q9pt69 xenopus lae
Q9ulk9 drosophula
Q9187 drosophula
Q9457 homo sapten
Q9471 pseudorable
Q9w451 drosophula
Q9w451 caulobacter
Q9w451 caulobacter
Q9w451 caulobacter
Q9hv5 pseudorable
Q9pv6 pseudorable
Q9pv6 pseudorable
Q9pv70 pseudorable
Q9pv8 homo sapten
Q9hb4 homo sapten
Q9h156 homo sapten
Q9nt26 homo sapten
Q9nt26 homo sapten
Q9nt28 preptomyce
Q13104 homo sapten
Q9h218 halobacteri

5 0003M2 5 0001K9 10 090451 5 090451 10 090451 11 091HR5 12 091HR5 12 091HR6 13 091HR4 14 091HR4 15 091HR4 16 091HR4 17 091HR4 18 091HR4 19 091HR4 10 091HR4 10 091HR4 10 091HR4 10 091HR4 11 091HR4 11 091HR4 12 091HR4 13 091HR4 14 091HR6 15 091HR4 16 091HR4 17 091HR4 18 091HR4 19 091HR4 19

83.5 83.5 83.5 83.5

113 94.5 93.5 88.5 85.5 85

# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_archeap:*

sp_vertebrate:* sp_rvirus:*
sp_bacteriap:*

sp_virus:*

sp_human:* sp_invertebrate:*

sp_mammal:*

sp_archea:*
sp_bacteria:*

sp_fungi:*

sp_organelle:*

sp_phage:* sp_mhc:*

sp_plant:* sp_rodent:*

	Description	Q9czs8 mus musculu	Q98tz1 qallus qall	Q9d7k8 mus musculu	093431 brachydanio	Q90yc5 brachydanio		Q923g4 rattus norv	Q9ptd0 ctenophorus			Q9puj4 gallus gall	090z32 brachydanio	Q9v4el drosophila	Q9u474 caenorhabdi	Q90z33 brachydanio	090z31 brachydanio
SUMMARIES	ID.	090288	098TZ1	Q9D7K8	093431	Q90YC5	Q9WUE7	092364	Q9PTD0	Q9PTD1	042304	Q9PUJ4	090232	Q9V4E1	090474	Q90Z33	090Z31
1	DB :::	11	13	7	13	13	11	11	13	13	13	13	13	Ŋ	Ŋ	13	13
:	Match Length DB	206	202	202	229	219	102	118	88	93	80	333	334	652	279	341	331
% Ouery	Match	81.7	44.0	30.2	29.4	28.9	24.5	24.2	19.9	19.4	17.2	15.5	15.3	14.5	14.0	13.2	12.6
	score	891.5	480	329.5	320.5	315	267.5	263.5	217.5	212	188	169.5	167	158.5	153	144.5	137.5
Result		П	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16

### ALIGNMENTS

09d571 mus musculu 098329 molluscum c Q9p107 homo sapien O35902 mus musculu O32232 bacillus su

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118 EFRPGETYYYISVPTPGSAGRCLKLRVSVCCRASTPEPLTEVPNSQPRGRGGPEGDAGSP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 WRGGDTPSPLCLLLLLLLL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                GGDTPSP 183
                                                                                   178 RDAAPIP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                         Q9D7K8
                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                           121 FPLGFEFLPGETYYYISVPTPESPGRCLRLQVSVCCKESGSSHESAHPVGSPGESGTSGW 180
                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                   118 FSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKS--ESAHPVGSPGESGTSGW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 PPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFG---HVQFSEKIQRFTPFSLGF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSE-----SAHPVGSPGESGTSGWR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Menzel P., Godement P., Dodelet V.C., Pasquale E.B.; "Ephrin-A6, a new ligand for EphA receptors in the developing visual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LLRTVLWAAFLGSPLRGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPG 65
                                                                                                                                                                                                                                                                       MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                                                                                                                                                                                                                                                                                                                                                        YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSL---PFGHVQFSEKIQRFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                 Š,
                                                                                                                                                                                         206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 480; DB 13; Leug.
Pred. No. 4e-41;
                                                                                                                                                                                         Length
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                             675E32971D1C6EBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91E2716FF91353F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                         11;
                                                                                                                                                                                       Score 891.5; DB 1
Pred. No. 4.3e-83;
                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 RGGDTPSPLCLLLLLLLLLLRLLRIL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
Pfam; PP00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
SEQUENCE 206 AA; 22859 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA; 22624 MW;
                                                                                                                                                                                       81.7%;
81.6%;
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InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1.
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2001 (TrEMBLrel. 18,
EPHRIN-A6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 51.9
97; Conservative
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                               168;
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SEQUENCE
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Matches
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RAA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RAA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Felischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Felischmann W., Staubii F., Sizuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubii F., Sizuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGES------GTSG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LWAPLIGICCSLAAADRHIVFWNSSNPKFREEDYTVHVQLNDYLDIICPHYEDDSVADAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP
                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK009144; BAB26102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 205;
                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADULT MALE TOWGE CONA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2310004315, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002533; Ephrin; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SEOUENCE 205 AA; 23772 MW; E37E55767459AEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,.2e-26;
78;
205 AA
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25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
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InterPro; IPR001799; Ephrin.
InterPro; IPR001680; WD40.
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25146 MW; 7191927.E03F8EA01 CRC64;
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   219 AA;
                                                                                             Query Match
Best Local Similarity
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Matches 54; Conserv
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SEQUENCE
   SEQUENCE
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                                                                                                                                                            Matches
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MEDLINE-21412237; PubMed=11520665;
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;

"Identification of ephrin-A3 and novel genes specific to the midbrain-MHB in embryonic zebrafish by ordered differential display.";

Mech. Dev. 107:83-96(2001).

EMBL; ABOS1678; BAB55891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 YESCOAEGPRAYK -- RWVCSLPFG-HV -- QFSEKIQRFTPFSLGFEFLPGETYYYISVPT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 SSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY-EGPGPPEGPETFALYMVDWPG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Durbin L., Briomi K., Cooke J.; L., Brennan C.H., Shiomi K., Cooke J.; "Eph signalling is required for segmentation and differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Crandata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ006838; CAA07264.1; -InterPro; IPR001799; Ephrin. InterPro; IPR033006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Province Pro
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 320.5; DB 350.0%; Pred. No. 8.7e-25
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                                                                                                                                                                                       229 AA
                                                                                                                                                                                                                                                                                                                                             EPHRIN A-L1.
Brachydanio rerio (Zebrafish) (Zebra danio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
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                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                       PRT;
: || :|| |-| 101 | :|| |-| 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101 | 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 50.09
Matches 67; Conservative
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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136 HHHGQECLRLKVDV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 PESSGQCLRLQVSV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
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01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN A3 (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                     83 YESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPE 139
                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                     24 SSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEG-PETFALYMVDWPG
                                                                                                                                  8
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  Length 219;
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EMBL; AF131912; AAD33515.1; -.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11838 MW; A497302F7FD7364B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ol-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Batting A-2 (FRAGNENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 267.5; DB 11;
Pred. No. 8.4e-20;
9; Mismatches 29; I
                                                  53;
28.9%; Score 315; DB 13;
43.1%; Pred. No. 3e-24;
iive 21; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTP 138
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                                                                                                                                                                                                                                                                                                          140 SSGQCLRLQVSVCCKERKSESAHP 163
                                                                                                                                                                                                                                                                                                                                                          138 HGRSCLRLRVYVCCSTASDSDDEP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5%; 55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                  62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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SEQUENCE FROM N.A. MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson S.; "The Pax protein Noi protein is required for commissural axon pathway
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
"Ephrin homologs are expressed in the adult lizard visual system.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF209776; AAF19443.1; -.
InterPro; IFF00179; Bphrin.
Pfo0812; Ephrin. 1.
ProDom; PF00812; Ephrin. 1.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danlo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.4%; Score 212; DB 13; Length 93; 45.6%; Pred. No. 3.5e-14; tive 16; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  formation in the rostral forebrain.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12028; CAR73391.1;
ZFIN; ZDB-GENE-0011281; efna5a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BD561F18D34C0F28 CRC64;
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                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN-A5 (FRAGMENT).
                                    93 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GPRAYKRWVCS---LPFGHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :||| |: || || 60 RMRGFKRWECNRPQSPDGPLRFSEKFQRFT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               93 93
93 AA; 11323 MW;
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Pfam; PF00812; Ephrin; I.
ProDom; PD002533; Ephrin; I.
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Matches 41; Conservative
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                                      PRELIMINARY;
                                                                                                                             EPHRIN A2 (FRAGMENT).
                                                                                                                                                  Ctenophorus ornatus.
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80 AA;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=95347;
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                                                                                                                                                                                                        Ctenophorus
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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                                    Q9PTD1
Q9PTD1;
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                     09PTD1
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                                                                                                                                                                                                                                                                                                                                 58 CPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQR 114
                                                                                                                                                                                                                                                                                                                                                                                                          115 FTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                        30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunlop S.A., Beazley L.D.;
expressed in the adult lizard visual system.";
to the EMBL/GenBank/DDBJ databases.
                                            Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A., Jimenez E., Varas A., Zapata A.G.;
"Expression and function of the Eph A receptors and their ligands ephrins A in the rat thymus.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX045577; AAK92219.1;
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                            24.2%; Score 263.5; DB 11; Length 118; 43.3%; Pred. No. 2.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 19.9%; Score 217.5; DB 13; Length 88; l Similarity 45.6%; Pred. No. 8.9e-15; 41; Conservative 13; Mismatches 31; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF209777; AAF19444.1; -...InterPro; IPR001199; Ephrin.
                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                 118 118
118 AA; 13470 MW; FF0277F079783A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 AA; 10636 MW; C56FCD8B13F219E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AA
                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 GPRAYKRWVCS---LPFGHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --QGFKRWECNRPHAPHSPIKFSEKFQRFT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, EPHRIN A3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                                52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN;
Chen P.B., Rodger J.,
"Ephrin homologs are e
Submitted (DEC-1999) t
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Best Local Similarity
                                                                                                                                                                                                                                                                             Local Similarity
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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NCBI_TaxID=10116;
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SEQUENCE
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SEQUENCE
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q9V4E1;
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                          ς;
                                                                RGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS 100
                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TKRPEQEAGING--KSSTISPFVKDHSGSSTDGSKAGHSSILGSEVALFAGIASGCIIFI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 KVDSKTVGQ-YEYYKVYMVDKDQADSCAIRKDNT-PLLNCAKPDQDVKFTIKFQEFSPNL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71; Gaps
                                                                                    18 IMVLWRTALAKSIVLDP------IYWNSSNPKFLPGQGLVLYPQIG--DKLDIICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 LGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVG----SPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 333;
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                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menzel P., Pasquale E.B.; "Coding sequence of chicken ephrin-B2."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF180795; AAD53948.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-B2.
4C28E8CB211B7783 CRC64;
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
    Pred. No. 8.1e-12;
3; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.5%; Score 169.5; DB 1
25.7%; Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
                                                                                                                                                                                                                                                                                       333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 -----ESGTSGWRGGDTPSPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA.
45.6%; Pred. No. tive 13; Mismatches
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                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36761 MW;
                                                                                                                                            101 LPF---GHVQFSEKIQRFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
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Best Local Similarity 25.73
Matches 64; Conservative
      Local Similarity 45.6
hes 36; Conservative
                                                                                                                                                                     | | ::|||| | || RPHSPNGPLKFSEKFQLFT
                                                                                                                                                                                                                                                                                     PRELIMINARY;
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28 3
333 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 LLLLILRLL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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        Best Loc
Matches
                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                 62
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Q90232
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Borkova D., Botchan M.R., Bouck J., Brokatein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 DWPGYESCQAEGPRAYKRWV----CSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYIS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKEQLETCHVT-----KSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIIS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                         MEDLINE=21290827; PubMed=11397014;
MEDLINE=21290827; PubMed=11397014;
Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
"Morphogenesis of prechordal plate and notochord requires intact
eph/ephrin b signaling.";
EMBL, 847375225; AAK64276.1;
EMBL, AF375226; AAK64276.1;
SEQUENCE 334 AA, 36998 MW; 341497E0FE9473BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TSNSTFEGLDNHHGGVCRSKSMKLVLRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 VPTP-----ESSGQC----LRLQVSVCCKERKSESAHPVGSP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDVSQIDSMQNGESGGKSGESVGSAGSDVALFAGVASGAVIFILIIIALVALL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 -----LLLLLLLLRLLRIL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dai Y., Kunes S.;
"Isolation and Characterization of Drosophila Ephrin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NAT-2000 (TIEMBLIEL. 13, Created)
01-CCT-2000 (TIEMBLIEL. 15, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
EPHRIN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // Match 15.3%; Score 167; DB 13;
Local Similarity 27.4%; Pred. No. 6.3e-09;
nes 64; Conservative 30; Mismatches 76;
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epidermal morphogenesis in C. elegans.";
                       Sell 99:781-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                         279 AA;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                    Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPHRIN B1
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A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

B Dodson K., Doup L.E., Downes M., Dugan-Roohs S., Dunkov B.C., Dunn P.,

R Durbin K.J. Evangelista C.C., Ferrar C., Ferriera S., Fleischmann W.,

R Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

R Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heilman T.J., Weil M. H., Ibegwam C.,

RA Harris N.L., Harvey D., Heilman T.J., Weil M. H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Krayitz S., Kulp D., Lai Z.,

RA Mimmel B.E., Kodira G.D., Kraft C., Krayitz S., Kulp D., Lai Z.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan N., Nelson B.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Syler E., Spradling A.C., Standers R.D.C., Scheeler F., Shan H.,

Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

RA Sheng X.H., Zahong F.N., Stupin G.M., Weissenbach J.,

RA Jens R. R.F., Zaveri J. S., Zhan M., Zhang G., Zhao O., Zheng L.,

RHEI, ALONG SH., Rubin G.M., Venter E., Wang S., Yao O.A.,

RY Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao O., Zheng L.,

RHEI, ALONG SH., Rubin G.M., Venter J.C.,

RHEI, ARCORSHI; AAFSB394.1; --

RHEI, REDORSHI; APFSB394.1; --

RHEI, REDORSHI; Behrin.

BRENE, PROBORIS; Ephrin.

BRENE, PROBORIS; Ephrin.
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 MHWNTSNSIFRIDNTDHIIDVNKGNLAFEFDQVHIICPVYE-PGTFENETEKYIIYNVSK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PGYESCQAEG--PRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 VYWNSSNP--RLLRGDAVVELGLN-----DYLDIVCPHYEGPGPPEG-PETFALYMVDW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=N2;
MEDLINR=20084449; PubMed=10619431;
Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
Chisholm A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5BA2F02F15964594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
Y37E11AR.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 158.5; DB 5;
; Pred. No. 1e-07;
25; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 DDLYRRIGGRCSTNNMKVVFKVCC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 ES----SGQC----LRLQVSVCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002533; Ephrin; 1.
SEQUENCE 652 AA; 72302 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         090474;
01-MAY-2000 (TrEMBLrel. 13, Cz
01-MAY-2000 (TrEMBLrel. 13, La
01-DEC-2001 (TrEMBLrel. 19, La
VAB-2 (HYPOTHETICAL PROTEIN Y3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%;
30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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90 GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 IYWNSTNPLVERYAAI-----GDTLDIVCPFFD-ENSDELTEQSIIYRVTEEEYENCERR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Evtinopteryyii; Neopterygii; Teleostel; Euteleostel; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE 21290827; Pubmed-11397014;
Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
"Morphogenesis of prechordal plate and notochord requires intact
eph/ephrin b signaling.";
Dev. Biol. 234:470-482(2001).
EMBL: AF375224; AAK64274.1; -.
FEMBL: AF375224; AAK64274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
8
                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF201079; AAF25647.1; -. EMBL; AC024759; AAK68436.1; -. InterPro; IRR01799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N., Maggi L.;
"The sequence of C. elegans cosmid Y37E11AR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phrin; 1.
32068 MW; 8C291A92D97D39EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 153; DB 5; 28.9%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 14.0%; Score 153; DB Best Local Similarity 28.9%; Pred. No. 1.4e-Matches 41; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA.
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 GLCASHNLKMVIHITDRNGDIG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00812; Ephrin; 1
ProDom; PD002533; Ephrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Direct Submission.";
Submitted (JUL-2001) t
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DB 13; Length 341;

13.2%; Score 144.5;

4 ;

Best Local Similarity 25.7%; Pred. No. 1.3e-06;

Matc	Matches	65; Conservative 26; Mismatches 89; Indels 73; Gaps	13;
οy	11	11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPG 65	
qq	12	12 LWILTAMCRYALPAAKSLESVV-WNSQNPKFVSGKGLVIYPEIGDKLDIICPKGDMGR 68	
Oy	99	66 PPEGPETFALYMVDWPGYESCQA-EGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEF 124	et
qa	69	69 PYEFYKLYLVKKEQAESCSTILDPNVLVTCNKPEKDIKFTIKFQEFSPNYMGLEF 123	м
Οy	125	088	1
qa	124	124 KRFTNYYITSTSNGTQEGLENREGGVCSTRSMKIIMKVGQDPNAPDPDLPDLPDRPYDNE 183	e
Qy	162	162HPVGSPG	10
qa	184	184 IKDPTTSPSRKTERGRENEVDGNGSKMPGKDTRNQNNSPGSVEGIFGSKPALFAAIGAGC 243	8
Qy	186	186 LLLLLLLLLRLL 198	
qq	244	34 VIFLIIILILIV 256	
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Search completed: September 28, 2002, 01:47:37 Job time: 642 sec

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